



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165011

TO: Joseph Voitach
Location: REM/2d51/2c18
Art Unit: 1632

Sept 12, 2005

Case Serial Number: 09/655109

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 07:52:31 ; Search time 3609.35 seconds
(without alignments)
9987.065 Million cell updates/sec

Title: US-09-655-109A-4

Perfect score: 947

Sequence: 1 accanaccacaaaagaagagagagatctatga 947

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68473088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854.8	90.3	895	7	CK230944 ILLUMIGEN
2	783.8	82.8	932	1	AJ816315
3	730	77.1	1436	3	AK033024 Mus muscu
C 4	724.8	76.5	799	7	CK774847
C 5	711.8	75.2	736	5	BM985193 UI-CF-EC1
6	673	71.1	707	5	BX924636 BX924636
C 7	656	69.3	726	7	CK777039 964031 MA
C 8	648.4	68.5	662	5	BQ015219 UI-H-ED1-
C 9	637.2	67.3	664	7	CK299391 UI-E-EU1-
C 10	631.2	66.7	650	5	BQ189224 UI-E-EU1-
C 11	617.6	65.2	642	2	BF116048 7n76908.x
C 12	613.2	64.8	621	1	A1627241 ty72a11.x
13	607.2	64.1	792	7	CN533672 UI-M-HN0-
14	604.8	63.9	784	7	CK635466 UI-M-HN0-
15	593	62.6	654	9	AY400131 Homo sapi
16	593	62.6	769	6	CA324092 UI-M-FY0-
17	589.6	62.3	718	7	CK636066 UI-M-HN0-
18	585.2	61.8	751	6	CB724087 UI-M-FY0-
19	580.2	61.3	639	6	CB444569 695860 MA
20	580	61.2	745	6	CD555761 UI-M-FY0-
C 21	575.2	60.7	618	4	BM312863 i980c01.x
C 22	574.4	60.7	723	7	CN457401 UI-M-HN0-
C 23	570.6	60.3	573	1	A1693196
24	568.6	60.0	610	6	CB287220 CMD55_C02

C 25	552	58.3	618	6	CB461283	721237 MA
C 26	551	58.2	573	1	AI912660	AI912660 wsl2c06.x
C 27	549.2	58.0	589	6	CB287224	CB287224 CMD55_C09
C 28	546.6	57.7	548	2	AW193683	AW193683 xm29d02.x
C 29	546.6	57.7	564	6	CB854840	UI-CF-EC1
C 30	546	57.7	576	1	AI693651	w479f12.x
31	543	57.3	703	7	CK639892	UI-M-HN0-
32	543	57.3	703	7	CN526226	UI-M-HN0-
33	542.8	57.3	798	5	BU704183	UI-M-F00-
34	541	57.1	700	7	CK640200	UI-M-HN0-
35	540.2	57.0	814	9	CG498682	OBT40156
C 36	539.2	56.9	547	1	AA725613	ai19d09.8
C 37	538.4	56.9	906	4	BI553612	603190533
38	537	56.7	695	5	BQ444213	UI-M-EX0-
39	536.2	56.6	770	9	CG499356	OST41345
C 40	535.4	56.5	539	2	BE464892	hv95d04.x
41	534.6	56.5	699	7	CO045489	UI-M-HO0-
42	534.6	56.5	839	6	CB989163	AGENCOURT
43	533.4	56.3	1940	3	CR603956	full-leng
44	533	56.3	778	3	CR626146	full-leng
45	531.2	56.1	604	6	CA751459	UI-M-F00-

ALIGNMENTS

RESULT 1
LOCUS CK230944 895 bp mRNA linear EST 09-DEC-2003
DEFINITION ILLUMIGEN MCQ_1331 Katze_MMPL2 Macaca mulatta cDNA 5' similar to human RYBP (Hs_7910), mRNA sequence.
ACCESSION CK230944
VERSION CK230944.1 GI:39637302
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 895)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magnus,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magnus
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2003.10.17. 765 Q20 bases. Assemblies in contig w/ 1 member(s). Contig contains 1 (0%) lib members.
PCR Primers
FORWARD: CCTCTACTAAGGGACAAA
BACKWARD: CACTATAGGCGAATTGGTA
Insert Length: 895 Std Error: 0.00
Plate: CL000013 row: C column: 06
Seq primer: CCTCTACTAAGGGACAAA
POLYA=Yes.

FEATURES

Location/Qualifiers
1. .895
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMPL2"
/notes="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #20400) and ZAP-cDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

Qy	28	TTGGATCTCTCGAGGCGACGAGGCGGAAACAGTGTGTAAGCCTTTTAAATGCAGCATCTG	87
Db	192	TTGGATTTGATGCTCTGCACTTTTAGAAACAGCGCGAAGCCTTTTAAATGCAGCATCTG	251
Qy	88	CGATGTGAGGAAGGCACTCCACGAGAAACCTCGGATCAATTTCTCAGCTGGTGGCNCA	147
Db	252	CGATGTGCGGAAGGCACTCCACGAGAAACCTCGCATCAATTTCTCAGCTGGTGGCACA	311
Qy	148	ACAAGTGGCAACAAGTATGCGACCCCAACACCCCTTAAAGAGGAGAGAGAGAAAGT	207
Db	312	GCAGTGGCACAGCAGTACGCCACTCCACCTCCCTTAAAGAGGAGAGAGAGAGGT	371
Qy	208	TGAAAGCAGACAGAAAGAACTGAGAAAGCAAGGAAATAGTCTAGTGTACCAA	267
Db	372	CGAAAGCCTTGACAAAGAAAGCCAGAGAAAGCAAGGACATTAGCCCCAGTGTACCAA	431
Qy	268	GAATAATACCAAGAAAGAAACCAACCAAGTGTGACATTTCTGAAAGATCCTCTAGTGA	327
Db	432	GAATAACACCAACCAAGAAACCAACCAAGTGTGATTTCTGAAAGATCCTCTAGTGA	491
Qy	328	AGCAACAGCATACAGTCTGCAATGCTACAACAAGACAGGCAACCAAAATCACACCTC	387
Db	492	AGCTAACAGCATACAGTCTGTAACGCTACAACAAGACAGGCAACCAAAATCACACCTC	551
Qy	388	AGGCCCGGCTGAATAACCTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGG	447
Db	552	AGGCCCGGCTGAAGAAATGTGACAGAGGACCGCACAGAGTTGGCAGTAACTGTGGG	611
Qy	448	CAACGTCACCGTCAATATACAGACTTTAAGGAAAGACTCGCTCCTCATCGACATCCTC	507
Db	612	CAACGTCACCGTCAATATACAGACTTTAAGGAAAGACTCGCTCCTCCTCCACATCCTC	671
Qy	508	ATCCAGTAGTCTCCAGTGCAGGCTGAGAACAGAGCAACAGACAGCTCGGGGTGAGA	567
Db	672	TTCCACAGTAGTCTCCAGTGCAGGCTGAGAACAGAGCAACAGACAGCTCGGGGTGAGA	731
Qy	568	GAGCAGACAGAGGCTCTCCGTTCTCCACGCAAGAGGCGACATGTCAGCAGTCAA	627
Db	732	GAGCAGACAGAGGCTCTCCGTTCTCCACGCAAGAGGCGACATGTCAGCAGTCAA	791
Qy	628	TGATGAATCTTTCTGAAATTTGCATGGAATTTGTGAAACTATGAATCAGGGTATGAAAT	687
Db	792	TGATGAATCTTTCTGAGATTTGCATGGAATTTGTG-AAAATGATCAGGGTATGAGAT	850
Qy	688	TCAAACTCTCACTGCTGCCATGTGCTTGATCGCTGCAATCTCTGTGGAGATCGAC	747
Db	851	TCAAACTCTCACTGCTGCCATGTGCTTGCA-CCCTGGAGAGTCTTCTGTGGA---CGAC	906
Qy	748	CTCTTAGTATGCTGCCAGGATATTTCTGCTTGCCATGGCATCTGGCCCAAGGAAT	807
Db	907	CTTGTAGTGACGCTTACCAGAGAGGTTCCGCTTGCCGTTGGCATCTGGCTACCAGGAAT	966
Qy	808	TTGCGACCTCTGACGATTTACTCTTGACATTTTATGATTTCCATTTTATATGATTTTC	867
Db	967	TTGCTACCTCTGACGATTTACTCTTGACATTTTATGATTTCCATTTTATATGATTTTC	1026
Qy	868	CTAACATATTTTATATATTTGATGTGCTCTCGAATCTACTTTTATATAAAAAA	920
Db	1027	CTAACATATTTTATATATTTGATGTGCTCTCGAATCTACTTTTATATATATA	1079

RESULT 4
CK774847/c
LOCUS 799 bp mRNA linear EST 20-FEB-2004
DEFINITION 963641 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK774847
VERSION CK774847.1 GI:42728990
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE	1	(bases 1 to 799)
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keel, J.W.	
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	
MEDLINE	21180013	
PUBMED	11282978	
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: 105 row: P column: 12 Seq primer: GTAATACGACTCACTATAGG. Location/Qualifiers 1..799 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 2BOV" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."	
FEATURES	source	
ORIGIN	Query Match 76.5%; Score 724.8; DB 7; Length 799; Best Local Similarity 94.9%; Pred. No. 2.3e-182; Matches 758; Conservative 1; Mismatches 39; Indels 1; Gaps 1; 116 AAACCTCGGATCAATTTCTCAGCTGGTGGCNCAACAGTGGCAACAGTATGCCACCCA 175 799 AAACCTCGGATCAATTTCCAGCTGGTGGCAACAGTGGCCCGCAGCAGTATGCCACTCCA 740 176 CCACCCCTTAAAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235 739 CCACCCCTTAAAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680 236 AAAGCAAGGAAATTAAGTCTTAGTGTACCAAGAAAAATACCAACAGAAAAACCAACCA 295 679 AAAGATAAGAAATTAAGTCTTAGTGTACCAAGAAAAATACCAACAGAAAAACCAACCA 620 296 AAGTCTGACATTTCTGAAAGATCCTCTAGTGAAGCAACAGCATAAGTGTGCAATGCT 355 619 AAGTCTGATATTCTGAAAGATCCTCTAGCAGAGTGAACAGTATACAGTCTGCAATGCT 560 356 ACACAAAG 415 559 ACACAAAG 500 416 AGCAGTGCACAGCAGTGGCAGTAACTGTGGGCAACGTCACCGTCAATTATCACAGACTTT 475 499 AGCAGCGCACAGCAGTGGCAGTGGCAGTGGGCAACGTCACCGTCAATTATCACAGACTTT 440 476 AAGGAAAAAGATCGCTCTCTCATCGACATCTCTCATCCAGTGACCTCCAGTGCAGGGTCA 535 439 AAGGAAAAAGATCGCTCTCTCTCGACATCTCTATCCACAGTGACCTCCAGTGCAGGGTCA 380 536 GAACAGCAGAAACAGAGCAGTTCGGGGTTCAGAGAGACAGAGAGAGAGAGAGAGAGAG 595 379 GAACAGCAGAAACAGAGCAGTTCGGGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320 596 TCCACGCCAAAGGGCGACATGTACAGAGTCAATGATGAATCTTTCTGAAATTCACATGG 655	

```

319 TCCAGGCAAAAGGCGAGCATGTGACGAGTAATGATGAGTCTTTTGAAGTGCACATGG 260
QY AATTGCAAACTATGATGAGGTATGAATTCAAACCTCCACCTGCCATGCTGCTT 715
Db AATTGCAAACTATGATGAGGTATGAATTCAAACCTCCACCTGCCATGCTGCTT 200
QY GCA-TCCTCGGAGATCTCTGTGGACATCGACTCTTCTAGTGATGCTGCCAGGATAATTT 774
Db GCACCCCTGGGAAATTTCTGTGGACATGACCTTTTGTAGTGATGCTGCCAGGATAATTT 140
QY CTGCTTCCATGGGCACTCTGGCCACCAAGAAATTCGACCCCTGACGATTAATTTGACA 834
Db TTGCTTCCATGGGCACTTTGGCCACCAAGAAATTCGACCCCTGACGATTAATTTGACA 80
QY CTTTATGATTAATCAATGTTTATATGATTTTCTTAACATCATTTATTAATGGATGTC 894
Db CTTTATGATTAATCAATGTTTATATGATTTTCTTAACATCATTTATTAATGGATGTC 894
QY TCCTGAATCTACTTTTAT 913
Db TCCTGAATCTACTTTTAT 1
QY 895 TCCTGAATCTACTTTTAT 913
Db 19 TCCTGAATCTACTTTTAT 1

RESULT 5
BM985193/c
LOCUS BM985193
DEFINITION UI-CF-EC1-acc-m-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-acc-m-16-0-UI 3', mRNA sequence.
ACCESSION BM985193
VERSION BM985193.1 GI:19611497
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-23, >AT rich/Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-acc-m-16-0-UI"
/tissue_type="Lung"
/dev_stages="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
```

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UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(ori)18 tail. The sequence tag for this library is
AAGTGCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 75.2%; Score 711.8; DB 5; Length 736;
Best Local Similarity 99.4%; Pred. No. 6.7e-179;
Matches 713; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 204 AAGTTGAAAGCAGGACAAAGAGAAACCTGAGAAACACGAAAGAAATAGTCTAGTGTTA 263
Db |||
QY 726 AAAGTGAAGCAGGACAAAGAGAAACCTTGAAGAAACGAAATTTAGTCTAGTGTTA 667
Db |||
QY 264 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323
Db |||
QY 666 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 607
Db |||
QY 324 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 383
Db |||
QY 606 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 547
Db |||
QY 384 CTTCAAGGCCCGGCTGAAACAGTGCAGAGGAGCACTGCACAGCAGTTCGGCAGTAATCG 443
Db |||
QY 546 CTTCAAGGCCCGGCTGAAACAGTGCAGAGGAGCACTGCACAGCAGTTCGGCAGTAATCG 487
Db |||
QY 444 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 503
Db |||
QY 486 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 427
Db |||
QY 504 CTTCAATCCACAGTGACCTCCAGTGCAGGAGTGCAGACAGCAACAGCAGCTCGGGGT 563
Db |||
QY 426 CTTCAATCCACAGTGACCTCCAGTGCAGGAGTGCAGACAGCAACAGCAGCTCGGGGT 367
Db |||
QY 564 CAGAGACACAGCAAAAGGGCTCTCCGCTTCCTCCAGCGCCAAAGGGGGGACATGTCAGCAG 623
Db |||
QY 366 CAGAGACACAGCAAAAGGGCTCTCCGCTTCCTCCAGCGCCAAAGGGGGGACATGTCAGCAG 307
Db |||
QY 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATG 683
Db |||
QY 306 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATG 247
Db |||
QY 684 AAATTCAAAACCTCCACCTGCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 743
Db |||
QY 246 AAATTCAAAACCTCCACCTGCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 187
Db |||
QY 744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAG 803
Db |||
QY 186 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAG 127
Db |||
QY 804 GAATTTGGCACCTGACGATTAATTTGACATTTTATGATTTATCCATTTTATATGAT 863
Db |||
QY 126 GAATTTGGCACCTGACGATTAATTTGACATTTTATGATTTATCCATTTTATATGAT 67
Db |||
QY 864 TTTCTCAACAAATCAATTAATTTGATGCTCTGCAATCTACTTTTTATAAAAAA 920
Db |||
QY 66 TTTCTCAACAAATCAATTAATTTGATGCTCTGCAATCTACTTTTTATAAAAAA 10
Db |||

RESULT 6
```

UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (ori)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 75.2%; Score 711.8; DB 5; Length 736;
Best Local Similarity 99.4%; Pred. No. 6.7e-179;
Matches 713; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 204 AAGTTGAAAGCAGGACAAAGAGAAACCTGAGAAACACGAAAGAAATAGTCTAGTGTTA 263
Db |||
QY 726 AAAGTGAAGCAGGACAAAGAGAAACCTTGAAGAAACGAAATTTAGTCTAGTGTTA 667
Db |||
QY 264 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323
Db |||
QY 666 CCAAGAAAAATACCAACAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 607
Db |||
QY 324 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 383
Db |||
QY 606 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGCAAAACAAATCA 547
Db |||
QY 384 CTTCAAGGCCCGGCTGAAACAGTGCAGAGGAGCACTGCACAGCAGTTCGGCAGTAATCG 443
Db |||
QY 546 CTTCAAGGCCCGGCTGAAACAGTGCAGAGGAGCACTGCACAGCAGTTCGGCAGTAATCG 487
Db |||
QY 444 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 503
Db |||
QY 486 TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGAGCTCGCTCTCATCGACAT 427
Db |||
QY 504 CTTCAATCCACAGTGACCTCCAGTGCAGGAGTGCAGACAGCAACAGCAGCTCGGGGT 563
Db |||
QY 426 CTTCAATCCACAGTGACCTCCAGTGCAGGAGTGCAGACAGCAACAGCAGCTCGGGGT 367
Db |||
QY 564 CAGAGACACAGCAAAAGGGCTCTCCGCTTCCTCCAGCGCCAAAGGGGGGACATGTCAGCAG 623
Db |||
QY 366 CAGAGACACAGCAAAAGGGCTCTCCGCTTCCTCCAGCGCCAAAGGGGGGACATGTCAGCAG 307
Db |||
QY 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATG 683
Db |||
QY 306 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACTATGAATCAGGGTATG 247
Db |||
QY 684 AAATTCAAAACCTCCACCTGCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 743
Db |||
QY 246 AAATTCAAAACCTCCACCTGCCATGCTGCTGCATCCCTCGGAGAAATCTTCTGTGGACAT 187
Db |||
QY 744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAG 803
Db |||
QY 186 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGGCCACCAG 127
Db |||
QY 804 GAATTTGGCACCTGACGATTAATTTGACATTTTATGATTTATCCATTTTATATGAT 863
Db |||
QY 126 GAATTTGGCACCTGACGATTAATTTGACATTTTATGATTTATCCATTTTATATGAT 67
Db |||
QY 864 TTTCTCAACAAATCAATTAATTTGATGCTCTGCAATCTACTTTTTATAAAAAA 920
Db |||
QY 66 TTTCTCAACAAATCAATTAATTTGATGCTCTGCAATCTACTTTTTATAAAAAA 10
Db |||

RESULT 6

Db 302 TGATGAATCTTCTGAAATTCACATGGAATGTGAAACCTATGAATCAGGGTATGAAT 243
Qy 688 TCAAAACCTCCACCTGCCATGCTGCTTGCATCCTCGAGAAATCTTCTGTGGACATCGAC 747
Db 242 TCAAAACCTCCACCTGCCATGCTGCTTGCATCCTCGAGAAATCTTCTGTGGACATCGAC 183
Qy 748 CTCTTAGTAGTCTGCCAGATAATTTCTGCTTGCATGCGCATCTGGCCACCAAGAAAT 807
Db 182 CTCTTAGTAGTCTGCCAGATAATTTCTGCTTGCATGCGCATCTGGCCACCAAGAAAT 123
Qy 808 TTGCACCCCTGACGATTACTCTTGACACTTTTATGATTTCCATTTTATATGATTTTC 867
Db 122 TTGCACCCCTGACGATTACTCTTGACACTTTTATGATTTCCATTTTATATGATTTTC 63
Qy 868 CTAACAATCATTTTATAATTTGGATGTGCTCTCGAATCTACTTTTATAAAAAA 920
Db 62 CTAACAATCATTTTATAATTTGGATGTGCTCTCGAATCTACTTTTATAAAAAA 10

RESULT 9
CK299391/c
LOCUS
DEFINITION
UI-E-EJ1-ajv-e-08-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajv-e-08-0-UI 3', mRNA sequence.
ACCESSION
CK299391
VERSION
CK299391.1 GI:39887700
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 664)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Greg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/eye.html
The following repetitive elements were found in this cDNA
sequence: 1-23, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .664
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajv-e-08-0-UI"
/tissue_types="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/notes="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (gt)¹⁸ tail. The
sequence tags for this library are: fetal eyes,
AGATCAAGA; lens, CGATAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCAATAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_ISSUE=human fetal eyes
TAG_LIB=UI-E-EJ1
TAG_SEQ=AGAATCAAGA"

ORIGIN
Query Match 67.3%; Score 637.2; DB 7; Length 664;
Best Local Similarity 99.2%; Pred. No. 5.7e-159;
Matches 639; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 277 CAACAGAAAAACCAAGTCTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAG 336
Db 653 CGAGGAGAAAAACCAAGTCTGACATTTCTGAAGATCTCTCTAGTGAAGCAACAG 594
Qy 337 CATACAGTCTGCAATGCTACAAAGACCGAGCAAAATCAACCTCAAGGCCCG 396
Db 593 CATACAGTCTGCAATGCTACAAAGACCGAGCAAAATCAACCTCAAGGCCCG 534
Qy 397 GCTGAAAAACGTGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGGGCAACCTCAC 456
Db 533 GCTGAAAAACGTGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGGGCAACCTCAC 474
Qy 457 CGTCATTATCACAGACTTTTAAGAAAAAGACTCGCTCTCATCGACATCTCTCAACAGT 516
Db 473 CGTCATTATCACAGACTTTTAAGAAAAAGACTCGCTCTCATCGACATCTCTCAACAGT 414
Qy 517 GACCTCCAGTGCAGGTCAGAACAGCAAGCAAGCAGCTCGGGTTCAGAGGACACAGA 576
Db 413 GACCTCCAGTGCAGGTCAGAACAGCAAGCAAGCAGCTCGGGTTCAGAGGACACAGA 354
Qy 577 CAAGGCTCTCTCCCGTTCTTCCACGCAAGGCGACATGTGAGCAGTCAATGATGAATC 636
Db 353 CAAGGCTCTCTCCCGTTCTTCCACGCAAGGCGACATGTGAGCAGTCAATGATGAATC 294
Qy 637 TTTCTGAAATTCACATGGAATTTGAAATCATGAAATCAGGGTATGAAATTCAAAACCT 696
Db 293 TTTCTGAAATTCACATGGAATTTGAAATCATGAAATCAGGGTATGAAATTCAAAACCT 234
Qy 697 CCACCTGCCATGCTGCTTGCATCCCTGAGAAATCTTCTGTGACATCGACCTCTTAGTG 756
Db 233 CCACCTGCCATGCTGCTTGCATCCCTGAGAAATCTTCTGTGACATCGACCTCTTAGTG 174
Qy 757 ATGCTGCCAGGATAATTTCTGCTTGCATGCGGCATCTGGCCACCAAGGAATTTTCGACCC 816
Db 173 ATGCTGCCAGGATAATTTCTGCTTGCATGCGGCATCTGGCCACCAAGGAATTTTCGACCC 114
Qy 817 TGAAGTACTCTTGACACTTTTATGATTTTATGATTTTATGATTTTCTTAAACATC 876
Db 113 TGAAGTACTCTTGACACTTTTATGATTTTATGATTTTCTTAAACATC 54
Qy 877 ATTATAATTTGATGTGCTCTGAAATCTACTTTTATAAAAAA 920
Db 53 ATTATAATTTGATGTGCTCTGAAATCTACTTTTATAAAAAA 10

RESULT 10
BQ189224
LOCUS
DEFINITION
UI-E-EJ1-ajv-e-08-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajv-e-08-0-UI 5', mRNA sequence.
ACCESSION
BQ189224
VERSION
BQ189224.1 GI:20364775
KEYWORDS
EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 650)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com).
The following repetitive elements were found in this cDNA
sequence: 626-650, >AT rich#Low_complexity (matched complement)
Seq primer: M13 REVERSE
FEATURES
source
Location/Qualifiers
1..650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajv-e-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pTTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATCGCGCAT; optic nerve, CCATTAAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
ORIGIN
Query Match 66.7%; Score 631.2; DB 5; Length 650;
Best Local Similarity 99.1%; Pred. No. 2.3e-157;
Matches 633; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 282 AGAAACCAACCAAGTCTGACATTCCTGAAGATCTCTCTAGTGAAGCAAGCATAC 341
Db 1 AGAAACCAACCAAGTCTGACATTCCTGAAGATCTCTCTAGTGAAGCAAGCATAC 60
QY 342 AGTCTGCAAAATGCTACCAAGACCGGCAACAAATCACACTCAAGGCCCGGTGA 401
Db 61 AGTCTGCAAAATGCTACCAAGACCGGCAACAAATCACACTCAAGGCCCGGTGA 120
QY 402 AAAACGTGGACAGGACACTGCACAGCAGTGTGGCAGTAACCTGTGGCAACGTCACCGTCA 461
Db 121 AAAACGTGGACAGGACACTGCACAGCAGTGTGGCAGTAACCTGTGGCAACGTCACCGTCA 180

QY 462 TTATCACAGACATTTTAAGGAAAAGACTCGCTCTCTCATCGACATCTCTCATCCACAGTGCCT 521
Db 181 TTATCACAGACATTTTAAGGAAAAGACTCGCTCTCTCATCGACATCTCTCATCCACAGTGCCT 240
QY 522 CAGTGCAGGCTCAGAACAGCAGAACACAGCAGCTCGGGTTCAGAGAGCAGACAGCAAGG 581
Db 241 CCAGTGCAGGCTCAGAACAGCAGAACACAGCAGCTCGGGTTCAGAGAGCAGACAGCAAGG 300
QY 582 GCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTCT 641
Db 301 GCTCTCCCGTTCTCCACGCCAAAGGGCGACATGTGACAGTCAATGATGAATCTTTCT 360
QY 642 GAAATTCACATGGAATTTGTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACC 701
Db 361 GAAATTCACATGGAATTTGTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACC 420
QY 702 TGCCCATGCTGCTGTCATCCCTGGAGAAATCTCTGTGGACATCGACTCTTAGTGATGCT 761
Db 421 TGCCCATGCTGCTGTCATCCCTGGAGAAATCTCTGTGGACATCGACTCTTAGTGATGCT 480
QY 762 GCCAGATATTTCTGCTTGCCATGGCATCTGCCACCAAGGAATTCGCACCTCGACG 821
Db 481 GCCAGATATTTCTGCTTGCCATGGCATCTGCCACCAAGGAATTCGCACCTCGACG 540
QY 822 ATTACTCTTGACACTTTTATGTATTCATTTTATATGATTTTCTTAACTCAATTTA 881
Db 541 ATTACTCTTGACACTTTTATGTATTCATTTTATATGATTTTCTTAACTCAATTTA 600
QY 882 TAATTGGATGTCCTCTGAATCTACTTTTATATAAAAAA 920
Db 601 TAATTGGATGTCCTCTGAATCTACTTTTATATAAAAAA 639
RESULT 11
BF116048/c
LOCUS
DEFINITION
7n76g08.x1 NCI CGAP Ov18 Homo sapiens CDNA clone IMAGE:3570638 3'
similar to TR:09UMW4 Q9UMW4 DEATH EFFECTOR DOMAIN-ASSOCIATED
FACTOR.; mRNA sequence.
BF116048
VERSION BF116048.1 GI:10985524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-xemall.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
1..642
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3570638"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"

/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st TGTACCAATCTGAAGTGGAGGCGCGGACATTTTCTTTTCTTTT 3"]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 65.2%; Score 617.6; DB 2; Length 642;
Best Local Similarity 98.9%; Pred. No. 9.9e-154;
Matches 631; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
Qy 277 CAACAAGAAACCAACCAAG-TCTGACATTTCTGAAGATCTCTTCTAGTGAAGCAACA 335
Db 638 CCAACAAGAAACCAACCAAGTTCTGACATTTTGAAGATCTCTTCTAGTGAAGCAACA 579
Qy 336 GCATACAGTCTGCAATGCTTACAACAAAGACCGAAACAAATCACACCTCAAGGCCCC 395
Db 578 GCATACAGTCTGCAATGCTTACAACAAAGACCGAAACAAATCACACCTCAAGGCCCC 519
Qy 396 GGCTGAAACCAAGTCTGACAGGACCTGCACAGCAGTTGGCAGTAACTGTGGCAACGTCA 455
Db 518 GGCTGAAACCAAGTCTGACAGGACCTGCACAGCAGTTGGCAGTAACTGTGGCAACGTCA 459
Qy 456 CCGTCATTATCACAGATTTAAGAAAGACTGCTCTCTCATCGACATCTCTATCCACAG 515
Db 458 CCGTCATTATCACAGATTTAAGAAAGACTGCTCTCTCATCGACATCTCTATCCACAG 399
Qy 516 TGACCTCCAGTGCAGGCTCGACAGCAGACCAAGCAGCTCGGGTTCAGAGCAGCAG 575
Db 398 TGACCTCCAGTGCAGGCTCGACAGCAGACCAAGCAGCTCGGGTTCAGAGCAGCAG 339
Qy 576 ACAAGGGCTCTCCCGTTCTTCCACGCAAGGGCGCATGTGACAGTCAATGATGAAT 635
Db 338 ACAAGGGCTCTCCCGTTCTTCCACGCAAGGGCGCATGTGACAGTCAATGATGAAT 279
Qy 636 CTTTCTGAAATTCGACATGGAATTTGAAACTATGAATCAGGATGAAATTCAAAC 695
Db 278 CTTTCTGAAATTCGACATGGAATTTGAAACTATGAATCAGGATGAAATTCAAAC 219
Qy 696 TCACCTGCCCATCTGCTGTCATCCCTGGAGATCTTCTGTGACATGACCTCTTAGT 755
Db 218 TCACCTGCCCATCTGCTGTCATCCCTGGAGATCTTCTGTGACATGACCTCTTAGT 159
Qy 756 GATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAGGAATTCGCACC 815
Db 158 GATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAGGAATTCGCACC 99
Qy 816 CTGACGATTAATCTTGAACATTTTATGATATGCAATTTTATGATATTTCTTAAACAT 875
Db 98 CTGACGATTAATCTTGAACATTTTATGATATGCAATTTTATGATATTTCTTAAACAT 39
Qy 876 CATTATAATGATGCTGCTGCAATCTACTTTTAT 913
Db 38 CATTATAATGATGCTGCTGCAATCTACTTTTAT 1

RESULT 12
AI627241/c
LOCUS
DEFINITION ty72411.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2284604 3, similar to TR:Q99710 Q99710 YY1-ASSOCIATED FACTOR 2. ;, mRNA
sequence.
ACCESSION AI627241
VERSION AI627241.1 GI:4664041
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

4/23/00

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 621)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio-llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 463.

FEATURES

source

1..621
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2284604"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 64.8%; Score 613.2; DB 1; Length 621;
Best Local Similarity 99.0%; Pred. No. 1.5e-152;
Matches 615; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 293 CCAAGTCTGACATCTGAAAGATCTCTCTAGTGAAGCAACAGCAGATACAGTCTGCAAT 352
Db 621 CCAAGTCTGACATCTGAAAGATCTCTCTAGTGAAGCAACAGCAGATACAGTCTGCAAT 562
Qy 353 GTTACAAACAAAGCAGCGAAACAAATCACCTCAAGGCCCCGGCTGAAAACCTGGAC 412
Db 561 GCTACAAACAAAGCAGCGAAACAAATCACCTCAAGGCCCCGGCTGAAAACCTGGAC 502
Qy 413 AGGAGCAGTGCACAGCAGTGGCAGTAACTGTGGCAAGCTCAGCTCATTTATCAGAC 472
Db 501 AGGAGCAGTGCACAGCAGTGGCAGTAACTGTGGCAAGCTCAGCTCATTTATCAGAC 442
Qy 473 TTTAAGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTACCTCCAGTGCAGG 532
Db 441 TTTAAGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTACCTCCAGTGCAGG 392
Qy 533 TCAGAACAGCAGAACCCAGAGCAGCTCGGGTTCAGAGAGCAGACAAAGGGCTCTTCCCGT 592
Db 381 TCAGAACAGCAGAACCCAGAGCAGCTCGGGTTCAGAGAGCAGACAAAGGGCTCTTCCCGT 322
Qy 593 TCCTCCACCCAAAGGGCGACATGTCCAGCTCAATGATGAATCTTCTGAAATTCGACA 652
Db 321 TCCTCCACCCAAAGGGCGACATGTCCAGCTCAATGATGAATCTTCTGAAATTCGACA 262
Qy 653 TGGAAATTGTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCATGCTG 712
Db 261 TGGAAATTGTGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCATGCTG 202
Qy 713 CTTGCAATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAAT 772
Db 201 CTTGCAATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAAT 142


```

773 TTCTGCTTGCATGGGCGATCTGGCCACCAAGGAATTTGCGACCTGACGATTACTCTTGA 832
Db      |||||
141 TTCTGCTTGCATGGGCGATCTGGCCACCAAGGAATTTGCGACCTGACGATTACTCTTGA 82
Qy      |||||
833 CACTTTATGATTCGATGTTGTTTATATGATTTCTTCAACAATCATTATTAATGGATGT 892
Db      |||||
81 CACTTTATGATTCGATGTTGTTTATATGATTTCTTCAACAATCATTATTAATGGATGT 22
Qy      |||||
893 GCTCTCGAATCTACTTTTAT 913
Db      |||||
21 GCTCTGAATCTACTATTTAT 1

RESULT 13
CN533672
LOCUS
DEFINITION
IMAGE:30655169 5', mRNA sequence.
CN533672
CN533672.1 GI:46861828
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 708-733, >AT_rich#Low_complexity
Seq primer: pYX-5.

FEATURES
source
1..792
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30655169"
/tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATGGAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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ORIGIN

```

Query Match      64.1%; Score 607.2; DB 7; Length 792;
Best Local Similarity 92.4%; Pred. NO. 6.3e-151;
Matches 671; Conservative 1; Mismatches 49; Indels 5; Gaps 3;
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195 AGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAATTAGTC 254
Db      |||||
1 AGAAGGAGAAAGTTGAAAAGCCTGCAAAAGAAAGCCAGAGAAAGCAAGGACATTAGCC 60
Qy      |||||
255 CTAGTGTATACCAAGAAAATACCAACAGAAACCAAAAGTCTGACATTCCTGAAG 314
Db      |||||
61 CCAGTGTACCAAGAAAACACCAACAGAAAACAAACAAAGTCTGATATTCGAAAG 120
Qy      |||||
315 ATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTCAACAAAGACGAGAAA 374
Db      |||||
121 ATCTCTCTAGTGAAGCTACAGCATACAGTCTGCTAACGCTACCAACAAAGACGAGAAA 180
Qy      |||||
375 CAAATCACACCTCAAGGCCCGGCTGAAAAAAGCTGACAGAGGACCTGCACAGCAGTTGG 434
Db      |||||
181 CAAACCAACCTCAAGGCCCGGCTGAAGAAATGTCAGCAGGACACCGCAGCAGTTGG 240
Qy      |||||
435 CAGTAATCTGGGCGACGTCACCGTCATTATACAGACTTTAAGGAAAAGACTCGCTCCT 494
Db      |||||
241 CAGTAATCTGGGCGAACGTCACCGTCATTATACAGACTTTAAGGAAAAGACTCGCTCCT 300
Qy      |||||
495 CATCGACATCTCTCATCCAGAGTGCCTCCAGTGCAGGGTCCAGAACAGCAGAGAACAGASCA 554
Db      |||||
301 CTCTCACATCTCTCTTCCACAGTGACCTCCAGTGCAGGGTCCAGAACAGCAGAGAACAGASCA 360
Qy      |||||
555 GCTCGGGGTCAGAGAGACAGACAGAGGGCTCTCCCGTCTCTCCAGCGCCAAAGGGCGACA 614
Db      |||||
361 GCTCGGGGTCAGAGAGACAGACAGAGGGCTCTCTCCCGTCTCTCCAGCGCCAAAGGGCGACA 420
Qy      |||||
615 TGTACAGCTCATGATGATCTTTCTGAAATGTCACATGGAATTTGTAAGAACTATGAAT 674
Db      |||||
421 TGTACAGCTCATGATGATGATCTTTCTGAGATTTGACATGGAATTTG-ANAATATGAAT 479
Qy      |||||
675 CAGGCTATGAAATTCAAAACCTCCAGTGCCTGCTTGCATCCCTGGAGAATCTTC 734
Db      |||||
480 CAGGCTATGAGATTCAAAACCTCCAGTGCCTGCTTGC-CCCTGGAGAGTCTTC 538
Qy      |||||
735 TGTGGACATCGACCTCTTAGTGTAGTGCAGAGATAATTTCTGCTGCCATGGGCACTGTG 794
Db      |||||
539 TGTGGA---CGACCTTGATTGACGCTACCCAGGAGAGGTTCCGCTTCCGCGGCACTGTG 595
Qy      |||||
795 GCACCAAGGAATTTCCGACCTCGACGATTTACTCTTGACACTTTTATGATTCATTTGT 854
Db      |||||
596 GCTACCAAGGAATTTCTGACCTTGACGATTTACTCTTGACACTTTTATGATTTCAITGTT 655
Qy      |||||
855 TTATATGATTTCTTAACAATCATTATTAATTTGATGCTCTCTGATCTACTTTTTTATA 914
Db      |||||
656 TTATATGATTTCTTAACAATCATTATTAATTTGATGCTCTCTGATCTACTTTTTTATA 715
Qy      |||||
915 AAAAAA 920
Db      |||||
716 TATATA 721

RESULT 14
CN534466
LOCUS
DEFINITION
IMAGE:30643452 5', mRNA sequence.
CN534466
CN534466.1 GI:41361332
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
```

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

The following repetitive elements were found in this cDNA

sequence: 704-729, >AT_rich#Low_complexity

FEATURES

Seq primer: pYX-5.
Location/Qualifiers
1. .784
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30643452"
/tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HNO"
/notes="Organ: Head; Vector: pYX-Asc; Site1: EcoR I;
Site2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATCTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 63.9%; Score 604.8; DB 7; Length 784;
Best Local Similarity 92.5%; Pred. No. 2.7e-150;
Matches 668; Conservative 1; Mismatches 48; Indels 5; Gaps 3;
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DB 1 GGAGAGGTGCAAAAGCTGCAGAAAGAAAGCCAGAGAAAGACAAAGGACATTAGGCCCCAG 60
QY 259 TGTACCAAGAAATACCAAGAGAAACCAAAACCAAGTCTGACATTCCTGAAAGATCC 318
DB 61 TGTACCAAGAAATACCAAGAGAAACCAAAACCAAGTCTGATATCTGAAAGATCC 120
QY 319 TCCTAGTGAAGCAACACAGCATACAGTCTGCAATGCTACAAAGAGACCAAGCCAGCAACAAA 378
DB 121 TCCTAGTGAAGCTAACAGCATACAGTCTGCAAGCTTACAAAGAGACCAAGCCAGCAACAAA 180
QY 379 TCACACCTCAAGGCCCGGCTGAAAGAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGT 438
DB 181 CCACACCTCAAGGCCCGGCTGAAAGATGTGGACAGGACACCGCACAGCAGTTGGCAGT 240
QY 439 AACTGTGGCAACGTCAACCGTCATTATCAAGACTTTAAGAAAGACTGCTCTCTATC 498
DB 241 AACTGTGGCAACGTCAACCGTCAATATACAGACTTTAAGAAAGACTGCTCTCTCTC 300
QY 499 GACATCTCTATCCACAGTGACCTCCAGTGCAGGGTCAAGACAGCAGAACACAGASCAGCTC 558
DB 301 CACATCTCTTCCACAGTGACCTCCAGTGCAGGGTCAAGACAGCAAGAACACAGAGCAGCTC 360
QY 559 GGGGTCAAGAGCAGACAGAGGGCTCTCCCGTTCTCTCCAGCGCAAGAGGGCGCAGATGTC 618
DB 361 GGGGTCAAGAGCAGACAGAGGGCTCTCCCGTCTCTCCAGCGCAAGAGGGCGCAGATGTC 420
QY 619 AGCAGTCAATGATGAATCTTCTGAATTTGCAATGGAATTTGGAAGACTATGATCAGG 678
DB 421 AGCAGTGAATGATGAATCTTCTGAGATTCACATGGAATTTGTTG-AAACTATGATCAGG 479
QY 679 GTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTTTCGATCCCTCGGAGAAATCTTCTGTG 738

DB 480 GTATGAGATTCAAACCTCCACCTGCCATGCTGTGCA-CCCTGGAGAGTCTTCTGTG 538
QY 739 GACATCGACCTCTTAGTAGTGTCCAGAGTAATTTCTGCTTGCCATGGGCATCTGGCCA 798
DB 539 GA---CGACCTTGTAGTGACGCTACCCAGGAGAGGTTCCGCTTGCCCGCATCTGGCTA 595
QY 799 CCAAGGAATTCGACCCCTGACGATTACTCTTGACACTTTTATGATATCCATTTGTTTAT 858
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QY 859 ATGATTTTCTTAACAATCAATTTATAATTTGATGCTGCTCTGATCTACTTTTATATAAAA 918
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QY 919 AA 920
DB 716 TA 717
RESULT 15
AY400131
LOCUS
DEFINITION
Homo sapiens RYBP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY400131
VERSION
AY400131.1 GI:39756120
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 654)
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 654)
AUTHORS
Todd M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment
FEATURES
Location/Qualifiers
source
1. .654
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>654
/gene="RYBP"
/locus_tag="HCM0455"
ORIGIN
Query Match 62.6%; Score 593; DB 9; Length 654;
Best Local Similarity 97.1%; Pred. No. 3.7e-147;
Matches 602; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 24 GGAATTCGGATCTCGAGGCCACGAAGCGGCGAAACAGTGTCTGAAGCTTTAAATGACGCA 83
DB 35 GGTTTTGGGATTCTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCTTTAAATGACGCA 94
QY 84 TCTGCCATGTGAGAAAGGACCTCCACCGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 143
DB 95 TCTGCCATGTGAGAAAGGACCTCCACCGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 154

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Qy 135 CCCATCATGACCATGGCGGCAAGAAGAGCCCGACAGGCGCAAAAAGACAAAGCGAAACC 194
Db 61 CCCATCATGACCATGGCGGCGCAAGAAGAGCCCGACAGGCGCAAAAAGACAAAGCGAAACC 120
Qy 195 TGGCGCAGACGAAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAACACAGTCTGAAGC 254
Db 121 TGGCGCAGACGAAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAACACAGTCTGAAGC 180
Qy 255 CTTTAAATGCAGCATCTCGCATGTGAGAAAGGCACCTCCACCAAGAAAACCTCGGATCAA 314
Db 181 CTTTAAATGCAGCATCTCGCATGTGAGAAAGGCACCTCCACCAAGAAAACCTCGGATCAA 240
Qy 315 TTCTCAGCTGGTGCGACAAACAAGTGGCAACAAGTATGCGCAACCCCAACCCCTTAAAAA 374
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Qy 375 GGAGAAGAGAGAAAGTTGAAAGCAGGACAGACAGAGAAACCTGAGAAAGACAGGAAT 434
Db 301' GGAGAAGAGAGAAAGTTGAAAGCAGGACAGACAGAGAAACCTGAGAAAGACAGGAAT 360
Qy 435 TAGTCCTAGTGTACCAAGAAAATACCAACAAGAAAACCAAAACCAAAAGTCTGACATCT 494
Db 361 TAGTCCTAGTGTACCAAGAAAATACCAACAAGAAAACCAAAACCAAAAGTCTGACATCT 420
Qy 495 GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACCAG 554
Db 421 GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACCAG 480
Qy 555 CGAAACAAATCACACCTCAAGGCCCGCGTGAAAGAGCTGACAGAGGACCTGCACAGCA 614
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Qy 615 GTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 674
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Qy 675 CTCCTCATGACATCTCTATCCAAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCA 734
Db 601 CTCCTCATGACATCTCTATCCAAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCA 660
Qy 735 GAGCAGCTCGGGTCAGAGAGCAGACAGAGGGCTCTCCGTTCTCCAGCCCAAGGG 794
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Db 721 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGAAAACTA 780
Qy 855 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTGGAGAA 914
Db 781 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTGCATCCCTGGAGAA 840
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Db 841 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGC 900
Qy 975 ATCTGGCCACCAAGGAATTTTCGACCCCTGCAGATTACTCTTGACACTTTTATGATTTCCA 1034
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Qy 1035 TTGTTTTATATGATTTTCTTAACAAATCATTTATTAATTTGGATGTGCTCTGAACTACTTT 1094
Db 961 TTGTTTTATATGATTTTCTTAACAAATCATTTATTAATTTGGATGTGCTCTGAACTACTTT 1020
Qy 1095 TTATAAAAA 1103
Db 1021 TAATAAAAA 1029

RESULT 2

US-10-956-157-1792

Sequence 1792, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1792
LENGTH: 1036
TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-1792

Query Match 90.1%; Score 1019.4; DB 21; Length 1036;
Best Local Similarity 99.4%; Pred. No. 2.9e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 75 CCACGAAGCGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
Db 1 CCGGACGGCGTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 60
Qy 135 CCATCATGACCATGGCGGCAAGAAGAGCCCGACAGGCCCAAAAAGACAAAGCGAAACC 194
Db 61 CCATCATGACCATGGCGGCAAGAAGAGCCCGACAGGCCCAAAAAGACAAAGCGAAACC 120
Qy 195 TGGCGCAGACGAAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAAAAACAGTCTGAAGC 254
Db 121 TGGCGCAGACGAAGGGTTTGGGATGTAGCGTCTGCACCTTCAGAAAAACAGTCTGAAGC 180
Qy 255 CTTTAAATGCAGCATCTCGCATGTGAGAAAGGCACCTCCACCAAGAAAACCTCGGATCAA 314
Db 181 CTTTAAATGCAGCATCTCGCATGTGAGAAAGGCACCTCCACCAAGAAAACCTCGGATCAA 240
Qy 315 TTCTCAGCTGGTGCGCAACAAGTGGCAACAAGTATGCGACCCCGACCGCTTAAAAA 374
Db 241 TTCTCAGCTGGTGCGCAACAAGTGGCAACAAGTATGCGACCCCGACCGCTTAAAAA 300
Qy 375 GGAGAAGAGAGAAAGTTGAAAGCAGGACAGAGAAACCTGAGAAAGACAGGAAT 434
Db 301 GGAGAAGAGAGAAAGTTGAAAGCAGGACAGAGAAACCTGAGAAAGACAGGAAT 360
Qy 435 TAGTCCTAGTGTACCAAGAAAATACCAACAAGAAAACCAAAACCAAAAGTCTGACATCT 494
Db 361 TAGTCCTAGTGTACCAAGAAAATACCAACAAGAAAACCAAAACCAAAAGTCTGACATCT 420
Qy 495 GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACCAG 554
Db 421 GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAATGCTTACAAACAAAGACCAG 480
Qy 555 CGAAACAAATCACACCTCAAGGCCCGCGTGAAAGAGCTGACAGAGGACCTGCACAGCA 614
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Db 541 GTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 600
Qy 675 CTCCTCATGACATCTCTATCCAAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCA 734
Db 601 CTCCTCATGACATCTCTATCCAAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCA 660
Qy 735 GAGCAGCTCGGGTCAGAGAGCAGACAGAGGGCTCTCCGTTCTCCAGCCCAAGGG 794
Db 661 GAGCAGCTCGGGTCAGAGAGCAGACAGAGGGCTCTCTCCGTTCTCCAGCCCAAGGG 720
Qy 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGAAAACTA 854
Db 721 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGAAAACTA 780

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QY 855 TGAATCAGGTATGAAATTCAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGAGAA 914
DB 781 TGAATCAGGTATGAAATTCAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGAGAA 840
QY 915 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTCTTGGCCATGGC 974
DB 841 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTCTTGGCCATGGC 900
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DB 901 ATCTGGCCACCAAGAAATTCGACCCCTGACGATTAATTTACTCTTGACACTTTTATGTATCCA 960
QY 1035 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGCTGCTCTGAATCTACTTT 1094
DB 961 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGCTGCTCTGAATCTACTTT 1020
QY 1095 TTATAAAAA 1103
DB 1021 TAATAAAAA 1029

RESULT 3
US-10-956-157-7027
; Sequence 7027, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7027
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7027

Query Match 90.1%; Score 1019.4; DB 21; Length 1036;
Best Local Similarity 99.4%; Pred. No. 2.9e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 75 CCACGAAGGCCTTTCTCTCCGAGCGCGCCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
DB 1 CCGGACGGGTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 60
QY 135 CCCATCCATGACATCGGCGACAGAAAGCCGACCGCCCAAAAGACAGCGAAACC 194
DB 61 CCCATCCATGACATCGGCGACAGAAAGCCGACCGCCCAAAAGACAGCGAAACC 120
QY 195 TGCAGCAGAGAGGTTTGGATGTCAGCTGCTGACCTTCAGAAACAGTCTGAAGC 254
DB 121 TGCAGCAGAGAGGTTTGGATGTCAGCTGCTGACCTTCAGAAACAGTCTGAAGC 180
QY 255 CTTTAAATGAGCATCTGGATGTAGGAAAGCCTCCACAGAAACCTCGGATCAA 314
DB 181 CTTTAAATGAGCATCTGGATGTAGGAAAGCCTCCACAGAAACCTCGGATCAA 240
QY 315 TTCTCAGCTGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAATAA 374
DB 241 TTCTCAGCTGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAATAA 300
QY 375 GGAGAGAGAGGAAAGTTGAAAGCAGGACAGAAAGAACCTTGAGAAAGACAGGAAT 434
DB 301 GGAGAGAGAGGAAAGTTGAAAGCAGGACAGAAAGAACCTTGAGAAAGACAGGAAT 360
QY 435 TAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCAAGTCTGACATTC 494
DB 361 TAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCAAGTCTGACATTC 420
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QY 495 GAAAGATCCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATCTCAACAAGAACGAG 554
DB 421 GAAAGATCCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATCTCAACAAGAACGAG 480
QY 555 CGAAACAAATCACACCTCAAGGCCCGCTGAAAGAGTGGACAGGAGCAGCTGCACAGCA 614
DB 481 CGAAACAAATCACACCTCAAGGCCCGCTGAAAGAGTGGACAGGAGCAGCTGCACAGCA 540
QY 615 GTTCGCACTAATCTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAAGACTCG 674
DB 541 GTTCGCACTAATCTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAAGACTCG 600
QY 675 CTCTCATCGACATCTCATCCACAGTGAACCTCAGTGCAGGGTCAGAAACAGCAGAAACA 734
DB 601 CTCTCATCGACATCTCATCCACAGTGAACCTCAGTGCAGGGTCAGAAACAGCAGAAACA 660
QY 735 GAGCAGCTCGGGGTGAGAGAGCAGACAGCAAGGGGCTCCCTCCGTTCCCTCCAGCCAAAGGG 794
DB 661 GAGCAGCTCGGGGTGAGAGAGCAGACAGCAAGGGGCTCCCTCCGTTCCCTCCAGCCAAAGGG 720
QY 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCACATCGCATGGAAATTTGAAAACTA 854
DB 721 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCACATCGCATGGAAATTTGAAAACTA 780
QY 855 TGAATCAGGGTATGAAATTCAAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAA 914
DB 781 TGAATCAGGGTATGAAATTCAAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAA 840
QY 915 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTCTTGGCCATGGGC 974
DB 841 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTCTTGGCCATGGGC 900
QY 975 ATCTGGCCACCAAGAAATTTCCGACCCCTGACGATTAATTTGACACTTTTATGTATCCA 1034
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QY 1035 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGCTGCTCTGAATCTACTTT 1094
DB 961 TTGTTTTATATGATTTTCTTAACAATCATTTATAATTTGATGCTGCTCTGAATCTACTTT 1020
QY 1095 TTATAAAAA 1103
DB 1021 TAATAAAAA 1029

RESULT 4
US-10-489-740-35
; Sequence 35, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis_PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-35

Query Match 90.1%; Score 1019.4; DB 21; Length 1128;
Best Local Similarity 99.4%; Pred. No. 3.1e-292;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 75 CCACGAAGGCCTTTCTCTCCGAGCGCGCCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
DB 85 CCGGACGGGTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 144
QY 135 CCCATCCATGACATCGGCGACAGAAAGCCGACCGCCCAAAAGACAGCGAAACC 194
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145 CCCATCCATGACCATGGCGCAAGAGAGCCGACAGGCGCAAAAGACAAAGCGAAACC 204
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255 CTTTAAATGACGATCTCGATGTGAGGAAAGGACCTCCACGAGAAACCTCGATCAA 314
265 CTTTAAATGACGATCTCGATGTGAGGAAAGGACCTCCACGAGAAACCTCGATCAA 324
315 TTCTCAGCTGTGGCACAACAAGTGGCAACAGTATGCCACCCACCCACCTCTAAAAA 374
325 TTCTCAGCTGTGGCGCAACAAGTGGCAACAGTATGCCACCCACCCACCTCTAAAAA 384
375 GGAGAAAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAT 434
385 GGAGAAAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAT 444
435 TAGTCCTAGTGTACCAAGAAATATCCAAAGAAACCAACCAAGTCTGACATTCT 494
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505 GAAAGATCCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACCAAAAGACCAG 564
555 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACCGTGACAGGACACTGCACAGCA 614
565 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACCGTGACAGGACACTGCACAGCA 624
615 GTTGGCAGTACTGTGGGCAAGCTCACCGTCAATTATCACAGACTTTAAGGAAAGACTCG 674
625 GTTGGCAGTACTGTGGGCAAGCTCACCGTCAATTATCACAGACTTTAAGGAAAGACTCG 684
675 CTCTCTATCGACATCTCTATCCACAGTGACCTCAGTGCAAGGCTCAGAAACAGCAGAACCA 734
685 CTCTCTATCGACATCTCTATCCACAGTGACCTCAGTGCAAGGCTCAGAAACAGCAGAACCA 744
735 GAGCAGCTCGGGGTGAGAGACAGACAGAGGGCTCTCCGTTTCTCCACGCGCAAGGG 794
745 GAGCAGCTCGGGGTGAGAGACAGACAGAGGGCTCTCCGTTTCTCCACGCGCAAGGG 804
795 CGACATGTCAGCAGTCAATGATGATCTTTTGTGAAATGTCATGGAATTTGTGAAACTA 854
805 CGACATGTCAGCAGTCAATGATGATCTTTTGTGAAATGTCATGGAATTTGTGAAACTA 864
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1035 TTGTTTTATATGATTTTCTTAACCAATCAATTTATATGGAATGTCCTGATCTACTTTT 1094
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1105 TTATAAAAA 1113
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RESULT 5
US-10-103-313-121
; Sequence 121, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-121

Query Match      82.7%; Score 935.8; DB 14; Length 2156;
Best Local Similarity 99.2%; Pred. No. 3.6e-267;
Matches 951; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

146 CCATGGCGCAAAAGAGAGCCGACAGGCGCAAAAGACAAAGCGAAACCTGCGCAGACG 205
1 CCACGCGTCCGAGAGAGAGCCGACAGGCGCAAAAGACAAAGCGAAACCTGCGCAGACG 60
206 AAGGGTTTTGGGATTGTAGCGTCTGCACTTTCAGAAACAGTGTGAAAGCCTTTAAATGCA 265
61 AAGGGTTTTGGGATTGTAGCGTCTGCACTTTCAGAAACAGTGTGAAAGCCTTTAAATGCA 120
266 GCATCTCGATGTGAGGAAAGGACCTCCACCA- GAAAACCTCGGATCAATTTCTCAGCTG 324
121 GCATCTCGATGTGAGGAAAGGACCTCCACCAAGTATGCCACCCACCCCTTAAAGAGTCTG 180
325 GTGSCACAACAAGTGGCACAACAGTATGCCACCCACCCCTTAAAGAGGAGAAAG 384
181 GTGSCACAACAAGTGGCACAACAGTATGCCACCCACCCCTTAAAGAGGAGAAAG 240
385 GAGAAAGTTGAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATTTAGTCTTAGT 444
241 GAGAAAGTTGAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAATTTAGTCTTAGT 300
445 GTTACCAAGAAAATATCCAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCCT 504
301 GTTACCAAGAAAATATCCAAAGAAACCAACCAAGTCTGACATTTCTGAAAGATCCT 360
505 CCTAGTGAACCAACAGCATACAGTCTGCAAAATGCTACAAAGACACGACGAAACAAAT 564
361 CCTAGTGAACCAACAGCATACAGTCTGCAAAATGCTACAAAGACACGACGAAACAAAT 420
565 CACACCTCAAGGCCCGGCTGAAAAACGTCGACAGGACACTGCACAGCAGTTGGCAGTA 624
421 CACACCTCAAGGCCCGGCTGAAAAACGTCGACAGGACACTGCACAGCAGTTGGCAGTA 480
625 ACTGTGGGCAACGTCACCGTCAATTATCAGACTTTTAAAGAAAGACTCGCTCTCATCG 684
481 ACTGTGGGCAACGTCACCGTCAATTATCAGACTTTTAAAGAAAGACTCGCTCTCATCG 540
685 ACATCTCTATCCACAGTGACCTCCAGTCAGGGTCAGAACAGACAGAACACAGAGCAGCTCG 744
541 ACATCTCTATCCACAGTGACCTCCAGTCAGGGTCAGAACAGACAGAACACAGAGCAGCTCG 600
745 GGGTCAGAGACGACAGAAAGGGCTCTCCGTTCTCCACGCGAAAGGGCGACATGTCA 804
601 GGGTCAGAGACGACAGAAAGGGCTCTCCGTTCTCCACGCGCAAAAGGGCGACATGTCA 660
805 GCAGTCAATGATGAATCTTTTGTGAAATTTGACATGGAATTTGTGAAACTATGATCAGGG 864
661 GCAGTCAATGATGAATCTTTTGTGAAATTTGACATGGAATTTGTGAAACTATGATCAGGG 720
865 TATGAAATTCAAAACCTCCACCTGCCCAGTCTGTCATCCCTGGAGAAATCTTCTGTGG 924
721 TATGAAATTCAAAACCTCCACCTGCCCAGTCTGTCATCCCTGGAGAAATCTTCTGTGG 780
925 ACATCGACCTCTTAGTGATGCTGCCAGGATAAATTTCTGCTTGCATGGGCAATCTGGCAC 984
781 ACATCGACCTCTTAGTGATGCTGCCAGGATAAATTTCTGCTTGCATGGGCAATCTGGCAC 840
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QY 985 CAAGGAATTTGGACCTGACGATTACTCTTGACACTTTTATGATTCATTTGTTTATA 1044
DB 841 CAAGGAATTTGGACCTGACGATTACTCTTGACACTTTTATGATTCATTTGTTTATA 900
QY 1045 TGATTTTCTCAACAATCAATTTATATATGATGATGCTCTGGAATCTACTTTTATAAAAA 1103
DB 901 TGATTTTCTCAACAATCAATTTATATATGATGATGCTCTGGAATCTACTTTTATAAAAA 959

RESULT 6
US-09-918-995-24859
; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24859
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(502)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-24859

Query Match 41.4%; Score 468.4; DB 10; Length 502;
Best Local Similarity 96.6%; Pred. No. 2.2e-128;
Matches 478; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 522 CATACAGTCTGCAATGCTAGCAACAGACGAGCAAAATCATCACTCAAGGCCCG 581
DB 8 CNAATAGATCGTATAGGCGCTCGAGGACGAGCAAAATCATCACTCAAGGCCCG 67
QY 582 GCTGAAACGTTGGACGAGCACTGACAGAGTTGGCAGTAATCTGGGCAAGCTCAC 641
DB 68 GCTGAAACGTTGGACGAGCACTGACAGAGTTGGCAGTAATCTGGGCAAGCTCAC 127
QY 642 CGTCATTATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCATCCACAGT 701
DB 128 CGTCATTATCACAGACTTTAAGGAAAGACTCGCTCTCATCGACATCTCATCCACAGT 187
QY 702 GACCTCCAGTGCAGGTGAGAACAGACGAGACGAGTCTGGGTGAGAGGACAGAGA 761
DB 188 GACCTCCAGTGCAGGTGAGAACAGACGAGACGAGTCTGGGTGAGAGGACAGAGA 247
QY 762 CAAGGCTCTCCGTTCTCCAGCGCCAAAGGCGGACATGTCAGCAGTCAATGATGATC 821
DB 248 CAAGGCTCTCCGTTCTCCAGCGCCAAAGGCGGACATGTCAGCAGTCAATGATGATC 307
QY 822 TTTGTGAATGTCACATGGAATTTGTAAGAACTATGAATCAGGGTATGAAATTCAGAACT 881
DB 308 TTTGTGAATGTCACATGGAATTTGTAAGAACTATGAATCAGGGTATGAAATTCAGAACT 367
QY 882 CCACCTGCCATGCTGCTGTCATGTCGAGAACTCTTCTGTCGACATGACACCTCTTAGTG 941
DB 368 CCACCTGCCATGCTGCTGTCATGTCGAGAACTCTTCTGTCGACATGACACCTCTTAGTG 427
QY 942 ATGCTGCCAGGATAATTTCTGTTGCCATGGGCACTGCGCCACCAAGGAATTTCCACCC 1001
DB 428 ATGCTGCCAGGATAATTTCTGTTGCCATGGGCACTGCGCCACCAAGGAATTTCCACCC 487
QY 1002 TGACGATTACTCTTG 1016

DB 488 TGACGATTACTCTTG 502

RESULT 7
US-09-764-848-12
; Sequence 12, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ08
; CURRENT APPLICATION NUMBER: US/09/764,848
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (621)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (626)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (658)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (712)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-848-12

Query Match 38.5%; Score 436; DB 9; Length 719;
Best Local Similarity 98.7%; Pred. No. 1.2e-118;
Matches 458; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
QY 157 AAGAAGAGCCCGACAGGCCCAAAAGACAGCGAAACCTGCGCAGAGCAAGGGTTTGG 216
DB 1 AAGAAGAGCCCGACAGGCCCAAAAGACAGCGAAACCTGCGCAGAGCAAGGGTTTGG 60
QY 217 GATTGTAGCGTCTGCACCTTCAGAAACAGTCTGAGGCTTTAATGAGCATCTGCGAT 276
DB 61 GATTGTAGCGTCTGCACCTTCAGAAACAGTCTGAGGCTTTAATGAGCATCTGCGAT 120
QY 277 GTGAGGAAGGCACCTCCACAGAAACCTCGGATCAATCTCAGCTGGTGCAACAA 336
DB 121 KTGAGGAAGGCACCTCCACAGAAACCTCGGATCAATCTCAGCTGGTGCAACAA 180
QY 337 GTGGCAACACAGTATGCCACCCACCCACCCCTAAAAAGGAGAGAGGAAAGTTGAA 396
DB 181 GTGGCAACACAGTATGCCACCCACCCACCCCTAAAAAGGAGAGAGGAAAGTTGAA 240
QY 397 AAGCAGGACAAAGAGAACCTTGAGAAACAGGAAATAGTCTTAGTTTACCAAGAA 456
DB 241 AAGCAGGACAAAGAGAACCTTGAGAAACAGGAAATAGTCTTAGTTTACCAAGAA 300
QY 457 AATACCAACAAAGAAACCAAAACCAAGTCTGACATCTTGAAAGATCTCTTAGTGAAGCA 516
DB 301 AATACCAACAAAGAAACCAAAACCAAGTCTGACATCTTGAAAGATCTCTTAGTGAAGCA 359
QY 517 AACGATACAGTCTGCAAAATGCTACAAAGACACGAGCAAGAAATCACAACCTCAAGG 576
DB 360 AACGATACAGTCTGCAAAATGCTACAAAGACACGAGCAAGAAATCACAACCTCAAGG 419
QY 577 CCCCAGGCTGAAAAACGT-GGACAGGAGCACTGACAGCAGTTGG 619
DB 420 CCCCAGGCTGAAAAACGTGGGACAGGAGCACTGACAGCAGTTGG 463

RESULT 8

US-10-116-016-12
; Sequence 12, Application US/10116016
; Publication No. US20030054379A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT208C1
; CURRENT APPLICATION NUMBER: US/10/116,016
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {621}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {626}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {643}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {658}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {712}
; OTHER INFORMATION: n equals a,t,g, or c
US-10-116-016-12

Query Match 38.5%; Score 436; DB 14; Length 719;

Best Local Similarity 98.7%; Pred. No. 1.2e-118;

Matches 458; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy	157	AAGAGAGCCCGACAGCCAAAGACAGCGAAACCTGCCGACAGAGGAGGTTTGG	216
Db	1	AAGAAGAGCCCGACAGCCAAAGACAGCGAAACCTGCCGACAGAGGAGGTTTGG	60
Qy	217	GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGCAGCATCTCGAT	276
Db	61	GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGCAGCATCTCGAT	120
Qy	277	GTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCAATTCCTAGCTGGTGACACAA	336
Db	121	KTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCAATTCCTAGCTGGTGACACAA	180
Qy	337	GTGGCACACAGTATGCCACCCACCCCTTAAAGGAGAGGAGGAGGAGTTGAA	396
Db	181	GTGGCACACAGTATGCCACCCACCCCTTAAAGGAGAGGAGGAGGAGTTGAA	240
Qy	397	AAGCAGGACAAAGAGAAACCTGAGAAAGACAGGAAATTTAGTCTAGTTTACCAAGAA	456
Db	241	AAGCAGGACAAAGAGAAACCTGAGAAAGACAGGAAATTTAGTCTAGTTTACCAAGAA	300
Qy	457	AATACCAACAGAAACCAACAAAGTCTGACATTTCTGAAAGATCTCTAGTGAAGCA	516
Db	301	AATACCAACAGAAACCAACAAAGTCTGACATTTCTGAAAGATCTCTAGTGAAGCA	359
Qy	517	AACAGCATACGTCTGCAATTCCTACAAAGACAGCGAAACCAAAATCACACCTCAAGG	576
Db	360	AACAGCATACGTCTGCAATTCCTACAAAGACAGCGAAACCAAAATCACACCTCAAGG	419
Qy	577	CCCCGGCTGAAAACGTTGGACAGGAGCAGTGCACAGCAGTTGG	619
Db	420	CCCCGGCTGAAAACGTTGGACAGGAGCAGTGCACAGCAGTTGG	463

RESULT 9

US-10-103-313-247
; Sequence 247, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PU207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {621}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {626}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {643}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {658}
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: {712}
; OTHER INFORMATION: n equals a,t,g, or c
US-10-103-313-247

Query Match 38.5%; Score 436; DB 14; Length 719;

Best Local Similarity 98.7%; Pred. No. 1.2e-118;

Matches 458; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy	157	AAGAAGAGCCCGACAGCCAAAGACAGCGAAACCTGCCGACAGAGGAGGTTTGG	216
Db	1	AAGAAGAGCCCGACAGCCAAAGACAGCGAAACCTGCCGACAGAGGAGGTTTGG	60
Qy	217	GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGCAGCATCTCGAT	276
Db	61	GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGCAGCATCTCGAT	120
Qy	277	GTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCAATTCCTAGCTGGTGACACAA	336
Db	121	KTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCAATTCCTAGCTGGTGACACAA	180
Qy	337	GTGGCACACAGTATGCCACCCACCCCTTAAAGGAGAGGAGGAGGAGTTGAA	396
Db	181	GTGGCACACAGTATGCCACCCACCCCTTAAAGGAGAGGAGGAGGAGTTGAA	240
Qy	397	AAGCAGGACAAAGAGAAACCTGAGAAAGACAGGAAATTTAGTCTAGTTTACCAAGAA	456
Db	241	AAGCAGGACAAAGAGAAACCTGAGAAAGACAGGAAATTTAGTCTAGTTTACCAAGAA	300
Qy	457	AATACCAACAGAAACCAACAAAGTCTGACATTTCTGAAAGATCTCTAGTGAAGCA	516
Db	301	AATACCAACAGAAACCAACAAAGTCTGACATTTCTGAAAGATCTCTAGTGAAGCA	359
Qy	517	AACAGCATACGTCTGCAATTCCTACAAAGACAGCGAAACCAAAATCACACCTCAAGG	576
Db	360	AACAGCATACGTCTGCAATTCCTACAAAGACAGCGAAACCAAAATCACACCTCAAGG	419
Qy	577	CCCCGGCTGAAAACGTTGGACAGGAGCAGTGCACAGCAGTTGG	619
Db	420	CCCCGGCTGAAAACGTTGGACAGGAGCAGTGCACAGCAGTTGG	463

RESULT 10
US-10-222-020-12
; Sequence 12, Application US/10222020
; Publication No. US20030175739A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT08C2
; CURRENT APPLICATION NUMBER: US/10/222,020
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/116,016
; PRIOR FILING DATE: 2003-04-05
; PRIOR APPLICATION NUMBER: 09/764,848
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
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; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,208
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR APPLICATION NUMBER: 60/249,212
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;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,264
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;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08

Query Match 38.5%; Score 436; DB 16; Length 719;

Best Local Similarity 98.7%; Pred. No. 1.2e-118;

Matches 458; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Qy 157 AAGAGAGCCGACAGGCGCAAAAGACAGGAACTGCGGACAGAGGAGGTTTGG 216
Db 1 AAGAGAGCCGACAGGCGCAAAAGACAGGAACTGCGGACAGAGGAGGTTTGG 60
Qy 217 GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGACGATCTGCCAT 276
Db 61 GATTGTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCTTTAAATGACGATCTGCCAT 120
Qy 277 GTGAGGAAGGCACCTCCACCAAGAAAACCTCGGATCAATTCTCAGCTGGTGCAACAA 336
Db 121 KTGAGGAAGGCACCTCCACCAAGAAAACCTCGGATCAATTCTCAGCTGGTGCAACAA 180

Qy 337 GTGGCACAACAGTATGCCACCCACCACCCCTCTAAAAGAGAGAAAGGAAAGTTGAA 396
Db 181 GTGGCACAACAGTATGCCACCCACCACCCCTCTAAAAGAGAGAAAGGAAAGTTGAA 240
Qy 397 AAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAATTAGTCTCTAGTGTTCACCAAGAA 456
Db 241 AAGCAGGACAAAGAGAAACCTTGAGAAAGACAAGGAAATTAGTCTCTAGTGTTCACCAAGAA 300
Qy 457 AATACCAACAAGAAACCAAAACCAAGTCTGACATTTCTGAAAGATCTCTCTAGTGAAGCA 516
Db 301 AATACCAACAAGAAACCAAAACCAAGTCTGACATTTCTGAAA-ATCCTCTCTAGTGAAGCA 359
Qy 517 AACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGACCAAAATCAACCTCAAGG 576
Db 360 AACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGACCAAAATCAACCTCAAGG 419
Qy 577 CCCCAGCTGAAAAACGT-GGACAGGAGCACTGACAGCAGTGG 619
Db 420 CCCCAGCTGAAAAACGTGGGACAGGAGCACTGACAGCAGTGG 463

RESULT 11

US-09-864-761-4575/c
; Sequence 4575, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

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; SEQ ID NO 4575
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012553.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
US-09-864-761-4575

Query Match      37.8%; Score 427.4; DB 9; Length 429;
Best Local Similarity 99.8%; Pred. No. 3.2e-116;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 586 AAAAAAGTGGACGAGCACTGCACAGCAGTTGGCAGTAATCTGTGGGCAACGTCACCGTC 645
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Db 429 AAAAAAGTGGACGAGCACTGCACAGCAGTTGGCAGTAATCTGTGGGCAACGTCACCGTC 370
   |||||

QY 646 ATTATCAGACACTTTAAGGAAAAGACTCGCTCTCATCGACATCCTCATCCACAGTGACC 705
   |||||
Db 369 ATTATCAGACACTTTAAGGAAAAGACTCGCTCTCATCGACATCCTCATCCACAGTGACC 310
   |||||

QY 706 TCAGTGCAGGCTCAGAACAGCAGACAGAGCAGCTCGGGGTGAGAGGACAGACAAAG 765
   |||||
Db 309 TCAGTGCAGGCTCAGAACAGCAGACAGAGCAGCTCGGGGTGAGAGGACAGACAAAG 250
   |||||

QY 766 GGTCTCTCCCGTTCTCTCCAGCCAAAGGCGCATGTGACAGTCAATGATCAATCTTTG 825
   |||||
Db 249 GGTCTCTCCCGTTCTCTCCAGCCAAAGGCGCATGTGACAGTCAATGATCAATCTTTG 190
   |||||

QY 826 TGAATTCACATGGAATTTGTGAACACTATGATCAGGTATGAAATTCAAAACCTCCAC 885
   |||||
Db 189 TGAATTCACATGGAATTTGTGAACACTATGAAATCAGGTATGAAATTCAAAACCTCCAC 130
   |||||

QY 886 CTGCCCATCTGCTTCATCTCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGC 945
   |||||
Db 129 CTGCCCATCTGCTTCATCTCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGC 70
   |||||

QY 946 TGCCAGGATAATTTCTGTTGCCATGGGCATCTGGCCACCAAGGAATTTGCAACCTGAC 1005
   |||||
Db 69 TGCCAGGATAATTTCTGTTGCCATGGGCATCTGGCCACCAAGGAATTTGCAACCTGAC 10
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QY 1006 GATTACTCT 1014
   |||||
Db 9 GATTACTCT 1
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RESULT 12
US-10-505-680-571
; Sequence 571, Application US/10505680
; Publication No. US20050095592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/357,031
; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 571
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(467)
; OTHER INFORMATION: "n" represents an unknown nucleotide
US-10-505-680-571

Query Match      29.8%; Score 337.4; DB 21; Length 467;
Best Local Similarity 91.4%; Pred. No. 2.1e-89;
Matches 424; Conservative 0; Mismatches 29; Indels 11; Gaps 6;

QY 75 CCACGAGGCGCTTTCTCTCCGAGCGCGCGCTTTTCGGCTTTGGGGGGGGGGGTACAG 134
   |||||
Db 5 CCCGAGCGCGTTCTCTCTCCGAGCGCGCGCTTTTCGGCTTTGGGGGGGGGGGTACAG 64
   |||||

QY 135 CCCATCCATGACCATGGGCGCAAGAAGAGCGCCGACGAGCCGCAAAAAGACCAAGCGAAACC 194
   |||||
Db 65 -CCATCCATGACCATGGGCGCAAGAAGAGCGCCGACGAGCCGCAAAAAGACCAAGCGAAACC 123
   |||||

QY 195 TGCCTCAGACCAAGGTTTTCGGGATTTAGCGTCTGCACCTTCAGAAAACAGTGTCTGAAGC 254
   |||||
Db 124 TGCCTCAGACCAAGGTTTTCGGGATTTAGCGTCTGCACCTTCAGAAAACAGTGTCTGAAGC 183
   |||||

QY 255 CTTTAAATGCAGCATCTCGCA-TGTGAGGAAAGGCACTCCACCAAGAAAACCTCGGATCA 313
   |||||
Db 184 CTTTAAATGCAGCATCTCGCACTGTGAGGAAAGGCACTCCACCAAGAAAACCTCGGATCA 243
   |||||

QY 314 ATTCTCAGCTGGTGACAAACAAGTGGCAACAAGTATGTCACACCCACCCCTTAAAA 373
   |||||
Db 244 ATTCTCAGCTGGTGACAAACAAGTGGCAACAAGTATGTCACACCCACCCCTTAAAA 303
   |||||

QY 374 AGGAGAAAGGAGGAAAGTTG-AAAAGCAGGACAAA---GAGAACTCTGAGAAAGACAA 428
   |||||
Db 304 AGGAGAAAGGAGGAAAGTTGAAAAGCAGGACAAAAGAGGAAANCTGAGAAAAGACCAA 363
   |||||

QY 429 GGAATATTAGTCC---TAGTGTGTACCAAGAAAATAACCAAGAAAACCAACCAAGTC 485
   |||||
Db 364 GGAATATTAGTCTTAGTTGTGTACCAAGAAAATAACCAAGAAAACCAACCAAGTC 423
   |||||

QY 486 TGACATTTGAAAGATCTCTCTAG-TGAAGCAAAACAGCATACAG 528
   |||||
Db 424 TGACATTTTGAAGATCTCTCTAGTTGAAGCAAAACAGCATACAG 467
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RESULT 13
US-10-505-680-570/c
; Sequence 570, Application US/10505680
; Publication No. US20050095592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC T
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/357,031
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 570
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(400)
; OTHER INFORMATION: "n" represents an unknown nucleotide
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US-10-505-680-570

Query Match	28.0%;	Score 316.6;	DB 21;	Length 400;
Best Local Similarity	93.5%;	Pred. No. 3.1e-83;		
Matches 375;	Conservative 0;	Mismatches 16;	Indels 10;	Gaps 4;
Qy	707	CCAGTGCAGGGTCC-AGAAACAGCAGCAAAACAGAGCAGCTCGGGGTCCAGAGAG-----CACAG	760	
Db	400	CCAGTGCAGGGTCAAGAAACAGCAGCAAAACAGAGCAGCTCGGGGTCCAGAGAGCACCAGC	341	
Qy	761	ACAAAGGCTCTCTCCCGTTCTCT--CCACAGCCAAAAGGGCGCAATCTCAGCAGTCAATGATG	817	
Db	340	AAAGGGCTCTCTCCCGTTCTCTTCNCAACCCCAAAGGGCGCAATCTCAGCAGTCAATGATG	281	
Qy	818	AATCTTTGTGAAATTCGACATGGAAATGTGAAAACCTATGAATCAGGGTATGAAATTCCAA	877	
Db	280	AATCTTTGTGAAATTCGACATGGAAATGTGAAAACCTATGAATCAGGGTATGAAATTCCAA	221	
Qy	878	ACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAATCTTCTGTGGACATCGACCTCTT	937	
Db	220	ACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAATCTTCTGTGGACATCGACCTCTT	161	
Qy	938	AGTGATGCTGCCAGGATAATTCTTCGCTTGCCATGGGCAATCTGGGCCCAAGGAATTTTCG	997	
Db	160	AGTGATGCTGCCAGGATAATTCTTCGCTT-NCATGGGCATCTGGGCCCAAGGAATTTTCG	102	
Qy	998	ACCTGACGATTACTCTTTGACACTTTTATGTATTCCATTGTTTATATGATTTTCCTTAAC	1057	
Db	101	ACCCTGAGGATTACTCTTTGACACTTTTATGTATTCCATTGTTTATATGATTTTCCTTAAC	42	
Qy	1058	AATCATTTATAATTGGATGTGCTCCTCGAATCTACTTTTAT	1098	
Db	41	AATCATTTATAATTGGATGTGCTCCTCGAATCTACTTTTAT	1	

RESULT 14

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US-10-242-535A-10941
; Sequence 10941, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(8)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-10941

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Query Match	25.3%;	Score	285.6;	DB	17;	Length	326;
Best Local Similarity	98.6%;	Pred. No.	4.6e-74;				
Matches	288;	Conservative	0;	Mismatches	4;	Indels	0;
Gaps	0;						
Qy	174	GCACAAAGACAAAGCGAAACCTGCCGACAGACGAAGGCTTTTGGGATGTTAGCGTCTGCAC	233				
Db	35	GGCACGAGGACAAAGCGAAACCTGCCGACAGACGAAGGCTTTTGGGATGTTAGCGTCTGCAC	94				
Qy	234	CTTCAGAAAACAGTGCTGAAGCCCTTAAATGACGACATCTGCGATGTGAGGAAGGCACCTC	293				
Db	95	CTTCAGAAAACAGTGCTGAAGCCCTTAAATGACGACATCTGCGATGTGAGGAAGGCACCTC	154				
Qy	294	CACCAGAAAAACCTCGGATCAATTTCTCAGCTGGTGGCCACCAACAGTGGCCACCAACAGTAGTATGC	353				
Db	155	CACCAGAAAAACCTCGGATCAATTTCTCAGCTGGTGGCCACCAACAGTGGCCACCAACAGTAGTATGC	214				
Qy	354	CACCCACACCCCTTAAAGGAGAGGAGAGAGTTGAAAGCAGGACCAAGAGAA	413				
Db	215	CACCCACACCCCTTAAAGGAGAGAGAGAGTTGAAAGCAGGACCAAGAGAA	274				
Qy	414	ACCTGAGAAAGACAAAGGAAATTAGTCTCTAGTGTTCACCAAGAAAAATACCAAC	465				
Db	275	ACCTGAGAAAGACAAAGGAAATTAGTCTCTAGTGTTCACCAAGAAAAATACCAAC	326				

RESULT 15

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US-10-085-783A-10941
; Sequence 10941, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-10941

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	Query Match	25.3%	Score 285.6;	DB 18;	Length 326;
	Best Local Similarity	98.6%;	Pred. No. 4.6e-74;		
	Matches 288;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	174	GC AAAAAGACAAGCGAAACTCGCGCAGACAGAAAGGTTTTGGCATGTGTAGCGTCTGCAC	233		
Db	35	GGCAGAGGACACAGCAAACTCGCGCAGACAGAGGTTTTGGGATGTGTAGCGTCTGCAC	94		
Qy	234	CTTCAGAAACAGTGCTCGAAGCCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTC	293		

Db	95	CTTCAGAAAACAGTGTCTGAAGCCTTTAAATGAGCATCTGCGATGTGAGAAAGGCACCTC	154
Qy	294	CACCGAAGAACTCGGATCAATTCTCAGCTGTGGCCACAAAGTGGCACACAGTATGC	353
Db	155	CACCGAAGAACTCGGATCAATTCTCAGCTGTGGCCACAAAGTGGCACACAGTATGC	214
Qy	354	CACCCACACACCCCTTAAAGGAGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAA	413
Db	215	CACCCACACACCCCTTAAAGGAGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAA	274
Qy	414	ACCTGAGAAAGACAAAGGAAATTAGTCTTAGTTACCAAGAAAAATACCAAC	465
Db	275	ACCTGAGAAAGACAAAGGAAATTAGTCTTAGTTACCAAGAAAAATACCAAC	326

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-655-109A-4
Perfect score: 947
Sequence: 1 accanaccccaaaaagaga.....tgccctcgagatctatga 947

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	944.2	99.7	947	6 AX114151	Sequence
3	944.2	99.7	947	6 AX138318	Sequence
4	944.2	99.7	947	6 AX138324	Sequence
5	883	93.2	1131	6 AX092139	Sequence
6	883	93.2	1131	6 AX138319	Sequence
7	883	93.2	1131	6 AX138332	Sequence
8	881.4	93.1	1131	6 AX114152	Sequence
9	871.2	92.0	2344	9 BC036459	Homo sapi
10	870	91.9	943	6 CQ1715417	Sequence
11	870	91.9	1021	9 AY228125	Homo sapi
12	870	91.9	1128	9 BC014959	Homo sapi
13	870	91.9	3641	6 BD209971	Human tra
14	868.4	91.7	1036	6 AX821956	Sequence
15	868.4	91.7	1036	9 AF179286	Homo sapi
16	866.8	91.5	4700	9 AB029551	Homo sapi
17	844	89.1	936	9 AF227959	Homo sapi
18	730	77.1	4394	10 BC053016	Mus muscu
19	730	77.1	4472	10 BC080287	Mus muscu

20	726.8	76.7	201844	2	AC132261	AC132261 Mus muscu
21	562.6	59.4	882	10	AF101779	AF101779 Mus muscu
22	545.6	57.6	549	9	HUMVI44E12	AF085840 Homo sapi
23	533.4	56.3	139207	2	AC069212	AC069212 Homo sapi
24	533.4	56.3	178219	9	AC104330	AC104330 Homo sapi
25	438.8	46.3	232891	2	AC117595	AC117595 Mus muscu
26	433.2	45.7	188281	2	AC121030	AC121030 Rattus no
27	433.2	45.7	229752	2	AC127045	AC127045 Rattus no
28	428.6	45.3	429	6	CQ053717	CQ053717 Sequence
29	428.6	45.3	429	6	CQ068876	CQ068876 Sequence
30	428.6	45.3	429	6	CQ095936	CQ095936 Sequence
31	428.6	45.3	429	6	CQ134678	CQ134678 Sequence
32	428.6	45.3	429	6	CQ173179	CQ173179 Sequence
33	428.6	45.3	429	6	CQ202367	CQ202367 Sequence
34	428.6	45.3	429	6	CQ217944	CQ217944 Sequence
35	428.6	45.3	429	6	CQ256519	CQ256519 Sequence
36	428.6	45.3	429	6	CQ293610	CQ293610 Sequence
37	428.6	45.3	429	6	CQ330531	CQ330531 Sequence
38	401.2	42.4	158041	2	AC140688	AC140688 Rattus no
39	232.4	24.5	253	6	CQ058707	CQ058707 Sequence
40	232.4	24.5	253	6	CQ078070	CQ078070 Sequence
41	232.4	24.5	253	6	CQ109071	CQ109071 Sequence
42	232.4	24.5	253	6	CQ147699	CQ147699 Sequence
43	232.4	24.5	253	6	CQ183070	CQ183070 Sequence
44	232.4	24.5	253	6	CQ207485	CQ207485 Sequence
45	232.4	24.5	253	6	CQ230949	CQ230949 Sequence

ALIGNMENTS

RESULT 1
AX092138
LOCUS AX092138 947 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 8 from Patent WO0116165.
ACCESSION AX092138
VERSION AX092138.1 GI:13444365

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Noteborn,M.H. and danen-van Oorschot,A.A.
TITLE Apoptin-associating protein
JOURNAL Patent: WO 0116165-A 8 08-MAR-2001;
LEADD B.V. (NL)

FEATURES
source
1..947
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature
1..947
/note="AAP-1-a nucleic acid wherein N can be A, C, G or T,"

ORIGIN

Query Match 99.7%; Score 944.2; DB 6; Length 947;
Best Local Similarity 100.0%; Pred. No. 1.4e-233;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACCNACCCCAAAAAGAGATCTGGATTCGGATTCCTCGAGGCCACGAGGCCGGAACAG 60
Dd 1 ACCNACCCCAAAAAGAGATCTGGATTCGGATTCCTCGAGGCCACGAGGCCGGAACAG 60
Qy 61 TCGTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGAAAGGACCTCTCCACGAGAAACC 120
Dd 61 TCGTGAAGCCTTTAAATGCGAGCATCTCGATGTGAGAAAGGACCTCTCCACGAGAAACC 120
Qy 121 TCGGATCAATCTCAGTGTGGCNCACAAAGTGGCAACAGTATGCGCCACCCACCACC 180
Dd 121 TCGGATCAATCTCAGTGTGGCNCACAAAGTGGCAACAGTATGCGCCACCCACCACC 180

[illegible]

	QY	661	TGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGTGCTTGTCATC	720
	DB	661	TGAAAACCTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGTGCTTGTCATC	720
	QY	721	CCTCGAGAATCTTCTGTGGACATCGACCCTTTAGTAGTGTGCAGGATAAATTTCTGCTT	780
	DB	721	CCTCGAGAATCTTCTGTGGACATCGACCCTTTAGTAGTGTGCAGGATAAATTTCTGCTT	780
	QY	781	GCCATGGGCATCTGGCCACCAAGGAATTTCCACCTCGACGATTACTCTTGACACTTTTA	840
	DB	781	GCCATGGGCATCTGGCCACCAAGGAATTTCCACCTCGACGATTACTCTTGACACTTTTA	840
	QY	841	TGTAATCCATTTGTTTTATATGATTTTCTTAACAATCATTTAATTTGGATGTGCTCTGA	900
	DB	841	TGTAATCCATTTGTTTTATATGATTTTCTTAACAATCATTTAATTTGGATGTGCTCTGA	900
	QY	901	ATCTACTTTTTATAAAAAGCCTTYGTGGCTCGAGAGTCTATGA	947
	DB	901	AICTACTTTTTATAAAAAGCCTTYGTGGCTCGAGAGTCTATGA	947
RESULT 4				
AXI38324				
LOCUS		AXI38324	947 bp	DNA linear PAT 30-MAY-2001
DEFINITION		Sequence 4 from Patent EP1081226.		
ACCESSION		AXI38324		
VERSION		AXI38324.1	GI:14274287	
KEYWORDS		Homo sapiens (human)		
SOURCE		Homo sapiens		
ORGANISM		Homo sapiens		
REFERENCE		1		
AUTHORS		Apoptin-associating protein		
TITLE		Patent: EP 1081226-A 4 07-MAR-2001;		
JOURNAL		Leadd B.V. (NL)		
FEATURES		Location/Qualifiers		
source		1..947		
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		/note="Description of Combined DNA/RNA Molecule: apoptin-associating protein"		
		misc_feature 54..920		
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ORIGIN				
		Query Match 99.7%; Score 944.2; DB 6; Length 947;		
		Best Local Similarity 100.0%; Pred. No. 1.4e-233;		
		Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
QY		1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATCTCGAGGCCACGAAGCCGGAACAG	60
DB		1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATCTCGAGGCCACGAAGCCGGAACAG	60
QY		61	TGCTGAAGCCTTTAAATGAGCATCTGCATGTGGAGAAAGCCACTCCACGAGAAACC	120
DB		61	TGCTGAAGCCTTTAAATGAGCATCTGCATGTGGAGAAAGCCACTCCACGAGAAACC	120
QY		121	TCGGATCAATTCAGCTGTGGCNCAACAAGTGGCACAAAGTATGCCACCCACCAACC	180
DB		121	TCGGATCAATTCAGCTGTGGCNCAACAAGTGGCACAAAGTATGCCACCCACCAACC	180
QY		181	CCCTAAAAAGGAGAGAGAGATTTGAAAAGCAGGACAAAGAGAACTTGAGAAAGA	240
DB		181	CCCTAAAAAGGAGAGAGAGATTTGAAAAGCAGGACAAAGAGAACTTGAGAAAGA	240
QY		241	CAAGGAAATTTAGTCTTAGTGTTCACGAGAAATATCCACACAGAAACCAACCAAGTC	300
DB		241	CAAGGAAATTTAGTCTTAGTGTTCACGAGAAATATCCACACAGAAACCAACCAAGTC	300
QY		301	TGACATCTTGAAAGATCTTCTAGTGAAGCAACAGATACAGTCTGCAAAATGCTACAC	360
DB		301	TGACATCTTGAAAGATCTTCTAGTGAAGCAACAGATACAGTCTGCAAAATGCTACAC	360
QY		361	AAAGACGAGCAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTTGGACAGGAC	420
DB		361	AAAGACGAGCAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTTGGACAGGAC	420
QY		421	TGCACAGCAGTGTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGATTTAAGA	480
DB		421	TGCACAGCAGTGTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGATTTAAGA	480
QY		481	AAAGACTCGCTCTCATCGACATCTTCATCCACAGTGACCTCCAGTGGAGGTCAGAAC	540
DB		481	AAAGACTCGCTCTCATCGACATCTTCATCCACAGTGACCTCCAGTGGAGGTCAGAAC	540
QY		541	GCAGAACGAGCAGCTCGGGGTGAGAGAGCAGCAAGAGGCTCTCCCGTTCCTCCAC	600
DB		541	GCAGAACGAGCAGCTCGGGGTGAGAGAGCAGCAAGAGGCTCTCCCGTTCCTCCAC	600
QY		601	GCCAAAGGGCGACATGTTCAGCAGTCAATGATGAATCTTTTGGAAATTCACATGAAATTG	660

Db 241 CAAGGAATTTAGTCTTAGTGTATTACCAAGAAAATATACCAACAAGAAACCAACAAAGTC 300
Qy 301 TGACATTTCTGAAGATCCTCTTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAC 360
Db 301 TGACATTTCTGAAGATCCTCTTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAC 360
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Db 841 TGTATTCATGTTTATATGATTTTCTCAACATCAATTTATTAATTTGGATGCTCTCTGA 900
Qy 901 ATCTACTTTTATAAAAAGCCCTTGTGGCCTCGAGAGATCTATGA 947
Db 901 ATCTACTTTTATAAAAAGCCCTTGTGGCCTCGAGAGATCTATGA 947

RESULT 5
AX092139
LOCUS AX092139 1131 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 9 from Patent WO0116165.
ACCESSION AX092139
VERSION AX092139.1 GI:13444366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Noteborn,M.H. and danen-van Oorschot,A.A.
TITLE Apoptin-associating protein
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Leadb B.V. (NL)
Patent: WO 0116165-A 9 08-MAR-2001;

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..1131
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ORIGIN
Query Match 93.2%; Score 883; DB 6; Length 1131;

Best Local Similarity 97.7%; Pred. No. 1e-217;
Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
Qy 24 GGAATTTGGATCCTCGAGGCCACGAAGGCGCAACAGTGTCTGAAGCCTTTAAATGACGA 83
Db 209 GGTTTTGGGATTTAGCGTCTGCACCTTCAGAAAACAGTGTCTGAAGCCTTTAAATGACGA 268
Qy 84 TCTGCCATGTGAGGAAGGCACCTCCACAGAAAACCTCGGATCAATTTCTCAGCTGCTGG 143
Db 269 TCTGCCATGTGAGGAAGGACCTCCACAGAAAACCTCGGATCAATTTCTCAGCTGCTGG 328
Qy 144 CACAAACAGTGGCACACAGTATGCCACCCCAACCCCTTAAAAAGGAGGAAGAGGA 203
Db 329 CACAAACAGTGGCACACAGTATGCCACCCCAACCCCTTAAAAAGGAGGAAGAGGA 388
Qy 204 AAGTTGAAAGCAGGACAAAGGAAACCTTGAGAAAGCAAGGAAATAGTCTTAGTGTTA 263
Db 389 AAGTTGAAAGCAGGACAAAGGAAACCTTGAGAAAGCAAGGAAATAGTCTTAGTGTTA 448
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Db 449 CCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCCTCCTA 508
Qy 324 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGCAAAATCACA 383
Db 509 GTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAGCAAAATCACA 568
Qy 384 CTTCAAGGCCCGGCTGAAAAAGCTGGACAGGAGCACTGCAAGAGTGGGAGTAACTG 443
Db 569 CTTCAAGGCCCGGCTGAAAAAGCTGGACAGGAGCACTGCAAGAGTGGGAGTAACTG 628
Qy 444 TGGGCAACCTGACCGTCAATATCACAGACTTTAAGGAAAAGACTCGCTCTCATCGACAT 503
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Qy 504 CTTCAATCCACAGTGAACCTCCAGTGCAGGGTTCAGAAACAGCAGAACCAAGCAGCTCGGGT 563
Db 689 CTTCAATCCACAGTGAACCTCCAGTGCAGGGTTCAGAAACAGCAGAACCAAGCAGCTCGGGT 748
Qy 564 CAGAGAGCAAGCAAGGGGCTCCCGTTCCTCCAGCGCAAGGGGAGCATGTGACGAG 623
Db 749 CAGAGAGCAAGCAAGGGGCTCCCGTTCCTCCAGCGCAAGGGGAGCATGTGACGAG 808
Qy 624 TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACATATGAATCAGGGTATG 683
Db 809 TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAAACATATGAATCAGGGTATG 868
Qy 684 AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACAT 743
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Db 929 CGACCTCTTAGTGATGCTGCGAGGATTAATTTCTGCTTGCATGGGAGCATCTGGCACCAG 988
Qy 804 GAATTTCCGACCTCGAGGATTAATTTCTGACACTTTTATGTTATCTGTTTATATGAT 863
Db 989 GAATTTCCGACCTCGAGGATTAATTTCTGACACTTTTATGTTATCTGTTTATATGAT 1048
Qy 864 TTTCTTAAACAATCATTTATAATTTGGATGCTCCTGAAATCTACTTTTTTAAAAAAGCC 923
Db 1049 TTTCTTAAACAATCATTTATAATTTGGATGCTCCTGAAATCTACTTTTTTAAAAAAGCC 1107
Qy 924 TTYGTGGCCTCGAGAGATCTATGA 947
Db 1108 TTYGTGGCCTCGAGAGATCTATGA 1131

RESULT 6
AX138319
LOCUS AX138319 1131 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 9 from Patent EP1083224.
ACCESSION AX138319


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Db 569 CCTCAAGGCCCCGGCTGAAACAACTGGACAGGACCACTGCACAGCAGTTCGGCAGTAAC TG 628
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Db 629 TGGGCAACGTCAACCGTCATTATATACACAGCTTTAAGGAAAAGACTCGCTCTCTATCGACAT 688
Qy 504 CCTCATCCACAGTACCTCCAGTCAGGTCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 563
Db 689 CCTCATCCACAGTACCTCCAGTCAGGTCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 748
Qy 564 CAGAGACACAGACAAAGGGCTCCCTCCGCTTCTCCACGCCAAAGGGGCGACATGTCAGCAG 623
Db 749 CAGAGACACAGACAAAGGGCTCCCTCCGCTTCTCCACGCCAAAGGGGCGACATGTCAGCAG 808
Qy 624 TCAATGATGAATCTTTCTGAAATTTGCACATGGAATTTGAAAACTATGAATCAGGGGTATG 683
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Db 929 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCACTCTGGCCACCAG 988
Qy 804 GAATTCGCAACCTCGACATTAATCTTTGACACTTTTATGATTTCCATGTTTATATGAT 863
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Qy 924 TTYGTGGCTCGAGAGATCTATGA 947
Db 1108 TTYGTGGCTCGAGAGATCTATGA 1131

RESULT 8
LOCUS AX114152 1131 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 5 from Patent EPI108785.
ACCESSION AX114152
VERSION AX114152.1 GI:14031160
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1.
AUTHORS
TITLE Apoptin-associating protein
JOURNAL Patent: Ep 1108785-A 5 20-JUN-2001;
Leadd B.V. (NL)
FEATURES
source location/Qualifiers
1. .1131
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .1131
/notes="AAP-1-b nucleic acid"

ORIGIN
Query Match 93.1%; Score 881.4; DB 6; Length 1131;
Best Local Similarity 97.6%; Pred. No. 2.6e-217;
Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;

Qy 24 GGAATTCGGATCTTCGAGGCCGAGAACAGCTGCTGAAGCCCTTTAATGAGCA 83
Db 209 GGTTTTGGGATGTGAGGCTGTGCACTTCAGAAACAGTGTGAGCCCTTTAATGAGCA 268
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Qy 204 AAGTTGAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAATTAGTCTTAGTGTGA 263
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Qy 264 CCAAGAAAAATACCAACAAGAAACCAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTA 323
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Qy 564 CAGAGACACAGACAAAGGGCTCCCTCCGCTTCTCCACGCCAAAGGGGCGACATGTCAGCAG 623
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Qy 624 TCAATGATGAATCTTTCTGAAATTTGCACATGGAATTTGTGAAAACTATGAATCAGGGTATG 683
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Db 929 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCACTCTGGCCACCAG 988
Qy 804 GAATTCGCAACCTCGACATTAATCTTTGACACTTTTATGATTTCCATGTTTATATGAT 863
Db 989 GAATTCGCAACCTCGACATTAATCTTTGACACTTTTATGATTTCCATGTTTATATGAT 1048
Qy 864 TTTCTTAACATCAATTTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
Db 1049 TTTCTTAACATCAATTTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy 924 TTYGTGGCTCGAGAGATCTATGA 947
Db 1108 TTYGTGGCTCGAGAGATCTATGA 1131

RESULT 9
LOCUS BC036459 2344 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens RING1 and YY1 binding protein, mRNA (cDNA clone MGC:33492 IMAGE:4813939), complete cds.
ACCESSION BC036459
VERSION BC036459.1 GI:22209025
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2344)
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LOCUS	CQ715417	943 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	Sequence 1351 from Patent WO02068579.				
ACCESSION	CQ715417				
VERSION	CQ715417.1	GI:42276274			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 1351 06-SEP-2002; PE Corporation (NY) (US)				
FEATURES	Location/Qualifiers				
source	1..943				
	/organism="Homo sapiens"				
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ORIGIN					
Query Match	91.9%; Score 870; DB 6; Length 943;				
Best Local Similarity	98.0%; Pred. No. 2.3e-214;				
Matches	879; Conservative 1; Mismatches 17; Indels 0; Gaps 0;				
Qy	24	GGAATTCGATCTCTCGAGGCCACGAGCGCGGAAACAGTGTGAAGCGCTTTAAATGCAGCA	83		
Db	42	GGTTTTGGGATTTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCGCTTTAAATGCAGCA	101		
Qy	84	TCGCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTCCTCAGCTGGTGG	143		
Db	102	TCTGCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTCCTCAGCTGGTGG	161		
Qy	144	CNCAACAAGTGGCAACAGTATGCCACCCACCCACCCCTTAAAGGAGGAAGAGAGA	203		
Db	162	CACAAACAAGTGGCAACAGTATGCCACCCACCCACCCCTTAAAGGAGGAAGAGAGA	221		
Qy	204	AAGTTGAAAAGCAGGCAAGAGAACTCTGAGAAAGCAAGGAAATTAGTCTTAGTGTTA	263		
Db	222	AAGTTGAAAAGCAGGCAAGAGAACTCTGAGAAAGCAAGGAAATTAGTCTTAGTGTTA	281		
Qy	264	CCAAGAAAAATACCAACAGAAAAACCAACCAAGTCTGACATCTGAAAGATCCTCCTA	323		
Db	282	CCAAGAAAAATACCAACAGAAAAACCAACCAAGTCTGACATCTGAAAGATCCTCCTA	341		
Qy	324	GTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAACAAAGACCGAGCAAAACAAATCACA	383		
Db	342	GTGAAGCAAAACAGCATACAGTCTGCAATGCTTACAACAAAGACCGAGCAAAACAAATCACA	401		
Qy	384	CCTCAAGGCCCGCGTGAAGAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACGT	443		
Db	402	CCTCAAGGCCCGCGTGAAGAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACGT	461		
Qy	444	TGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAAGACTCGCTCTCATCGACAT	503		
Db	462	TGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAAGACTCGCTCTCATCGACAT	521		
Qy	504	CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCCAGCAGCTCGGGGT	563		
Db	522	CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAAACAGCAGAACCCAGCAGCTCGGGGT	581		
Qy	564	CAGAGAGCACAGAACAGGGCTCTCCGGTTCTCTCCACGCGCAAGGGCGACATGTCCAGCAG	623		
Db	582	CAGAGAGCACAGAACAGGGCTCTCCGGTTCTCTCCACGCGCAAGGGCGACATGTCCAGCAG	641		
Qy	624	TCAATCATGAATCTTTCTGAAATGACATGGAAATTTGTGAAACTATGAAATCAGGGTATG	683		
Db	642	TCAATCATGAATCTTTCTGAAATGACATGGAAATTTGTGAAACTATGAAATCAGGGTATG	701		
Qy	684	AAATTCAAACCTCCACCTGCCCATGCTGCTTGCATCCCTCGGAGAAATCTTCTGTGGACAT	743		

Db	702	AAATTCAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACAT	761		
Qy	744	CGACCTCTTAGTAGTGTGCGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG	803		
Db	762	CGACCTCTTAGTAGTGTGCGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG	821		
Qy	804	GAAATTCGCACCTCGACGATTACTCTTGACACTTTTATGTATGTATTCATGTTTATATGAT	863		
Db	822	GAAATTCGCACCTCGACGATTACTCTTGACACTTTTATGTATGTATTCATGTTTATATGAT	881		
Qy	864	TTTCTCTTACCAATCAATTATAATTTGGATGTGCTCTCGAATCTACATCTTTTATAAAAAA	920		
Db	882	TTTCTCTTACCAATCAATTATAATTTGGATGTGCTCTCGAATCTACATCTTTTATAAAAAA	938		
RESULT 11					
AY228125	1021 bp mRNA linear PRI 12-MAY-2004				
LOCUS	AY228125				
DEFINITION	Homo sapiens apoptin-associating protein 1 (AAP1) mRNA, complete cds.				
ACCESSION	AY228125				
VERSION	AY228125.1				
GI	29423710				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1021)				
AUTHORS	Danen-van Oorschot, A.A.M., Voskamp, P., Seelen, M.C., van Miltenburg, M.H., Bolk, M.W., Tait, S.W., Boesen-de Cock, J.G., Rohn, J.L., Borst, J. and Noteborn, M.H.				
TITLE	Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell killing				
JOURNAL	Cell Death Differ. 11 (5), 564-573 (2004)				
PUBMED	14765135				
REFERENCE	2 (bases 1 to 1021)				
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.				
TITLE	AAP-1, a binding partner of Apoptin, induces cell death in human tumor cells but not in normal diploid cells				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 1021)				
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.				
TITLE	Direct Submision				
JOURNAL	Submitted (31-JAN-2003) Leadd BV, Wassenaarseweg 72, Leiden 2333 AL, The Netherlands				
FEATURES	Location/Qualifiers				
source	1..1021				
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	/cell_type="Epstein-Barr virus-transformed lymphocytes"				
gene	1..1021				
	/gene="AAP1"				
CDS	64..744				
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	/note="AAP-1; DEDAF/YEAF1; similar to RYBP and YAF2"				
	/codon_start=1				
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	/protein_id="AAO73587.1"				
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Db	702	AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACAT	761
Qy	744	CGACCTCTTAGTATGCTGCGAGGATAAATTTCTGCTTGCATGGGCACTGGCCACCAAG	803
Db	762	CGACCTCTTAGTATGCTGCGAGGATAAATTTCTGCTTGCATGGGCACTGGCCACCAAG	821
Qy	804	GAAATTCGCACCTCGACGATTACTCTTGACACTTTTATGATTTCCATTGTTTATATGAT	863
Db	822	GAAATTCGCACCTCGACGATTACTCTTGACACTTTTATGATTTCCATTGTTTATATGAT	881
Qy	864	TTTCTTAAACAATCATTATATAATTTGGATGCTGCTCGAATCTACTTTTATAAAAAA	920
Db	882	TTTCTTAAACAATCATTATATAATTTGGATGCTGCTCGAATCTACTTTTATAAAAAA	938
RESULT 11			
LOCUS	AY228125	1021 bp	mRNA linear PRI 12-MAY-2004
DEFINITION	Homo sapiens apoptin-associating protein 1 (AAP1) mRNA, complete cds.		
ACCESSION	AY228125		
VERSION	AY228125.1 GI:29423710		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1021) Danen-van Oorschot, A.A.M., Voskamp, P., Seelen, M.C., van Miltenburg, M.H., Bolk, M.W., Tait, S.W., Boesen-de Cock, J.G., Rohn, J.L., Borst, J. and Noteborn, M.H.		
TITLE	Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell killing		
JOURNAL	Cell Death Differ. 11 (5), 564-573 (2004)		
PUBMED	14765135		
REFERENCE	2 (bases 1 to 1021)		
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.		
TITLE	AAP-1, a binding partner of Apoptin, induces cell death in human tumor cells but not in normal diploid cells		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1021)		
AUTHORS	Danen-van Oorschot, A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JAN-2003) Leadd BV, Wassenaarseweg 72, Leiden 2333 AL, The Netherlands		
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ACCESSION	BD209971
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KEYWORDS	JP 2002513554-A/43.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Hillman,J.L., Bandman,O., Lal,P., Yue,H., Reddy,R., Tang,T.Y., Gerstin,E.H., Patterson,C., Baughn,M.R., Azimzai,Y. and Lu,D.A.M.
TITLE	Human transcriptional regulator molecules
JOURNAL	Patent: JP 2002513554-A 43 14-MAY-2002;
COMMENT	INCYTE PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002513554-A/43 PD 14-MAY-2002 PF 04-MAY-1999 JP 2000547113 PR 05-MAY-1998 US 60/084254, 07-AUG-1998 US 60/095827 PR 02-OCT-1998 US 60/102745 PI JENNIFER L HILLMAN,OLGA BANDMAN,PREETI LAL,HENRY YUE,ROOPA PI REDDY, PI TOM Y TANG,EDWARD H GERSTIN,CHANDRA PATTERSON,MARIAH R BAUGHN, PI YALDA AZIMZAI,DYUNG AINA M LU PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/02,A61P43/00, PC C07K14/47, PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68//C12P21/ PC 02, PC C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC Incyte clone 3149729CB1 FH Key Location/Qualifiers FT source 1..3641 FT /organism='Homo sapiens (human)'. FT Location/Qualifiers FT 1..3641 FT /organism='Homo sapiens' FT /mol_type='genomic DNA' FT /db_xref='taxon:9606'
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ACCESSION AX821956
VERSION AX821956.1 GI:39725177
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
TITLE Method to modify differentiation of pluripotential stem cells
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zheng, L., Schickling, O., Peter, M.E. and Lenardo, M.J.
TITLE The death effector domain-associated factor plays distinct
regulatory roles in the nucleus and cytoplasm
JOURNAL J. Biol. Chem. 276 (34), 31945-31952 (2001)
MEDLINE 21402885
PUBMED 11395500
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REFERENCE	2 (bases 1 to 1036)	
AUTHORS	Zheng,L.X., Yoo,T. and Lenardo,M.J.	
TITLE	A novel protein associated with Caspase-10 DED domain	
JOURNAL	Unpublished	
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AUTHORS	Zheng,L.X., Yoo,T. and Lenardo,M.J.	
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	26	357.4	37.7	719	4	AA850003	Aas85003 cDNA enco
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	28	357.4	37.7	719	10	ADC46161	Adc46161 Human neo
C	30	317.8	33.6	400	10	ADK61400	Adk61400 Ovarian c
C	30	255.8	27.0	515	5	AAS80294	Aas80294 DNA enco
C	31	232.4	24.5	253	4	AAI23937	Aai23937 Probe #13
C	32	232.4	24.5	253	4	ABA69056	Aba69056 Human foe
C	33	232.4	24.5	253	4	AAI49244	Aai49244 Probe #17
C	34	232.4	24.5	253	4	ABA51067	Aba51067 Human bre
C	35	232.4	24.5	253	4	ABA36000	Aba36000 Probe #14
C	36	232.4	24.5	253	4	AAK43164	Aak43164 Human bon
C	37	232.4	24.5	253	4	AAK17369	Aak17369 Human bra
C	38	232.4	24.5	253	4	ABS42798	Abs42798 Human liv
C	39	232.4	24.5	253	5	AAI09536	Aai09536 Probe #95
C	40	232.4	24.5	253	6	ABS17240	Abse17240 Human gen
C	41	197.8	20.9	467	10	ADK61401	Adk61401 Ovarian c
C	42	167.4	17.7	470	4	AAI13037	Aai13037 Probe #29
C	43	167.4	17.7	470	4	ABA54738	Aba54738 Human foe
C	44	167.4	17.7	470	4	AAI34388	Aai34388 Probe #30
C	45	167.4	17.7	470	4	ABA44285	Aba44285 Human bre

ALIGNMENTS

RESULT 1
Aaf55595
ID Aaf55595 standard; cDNA; 947 BP.

AC Aaf55595;

XX 29-MAY-2001 (first entry)

XX Nucleotide sequence of apoptin-associating protein 1 cDNA clone a.

XX Apoptin-associating protein; AAP; apoptosis; cell proliferation;
cell death; autoimmune disease; cancer; ss.

XX Homo sapiens.

XX W0200116165-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-NL000612.

XX 02-SEP-1999; 99EP-00202858.

XX 21-OCT-1999; 99EP-00203465.

XX (LEAD-) LEADD BV.

XX Noteborn MHM, Danen-Van Oorschot AAAM;

XX WPI; 2001-235090/24.

XX New nucleic acids encoding apoptin-associating proteins useful for
inducing apoptosis, particularly p53 independent apoptosis, or for
treating cancers or autoimmune diseases.

XX Claim 6; Fig 1; 50pp; English.

XX The present sequence encodes a human apoptin-associating protein 1
(AAP1). The protein is capable of providing apoptosis. AAP polypeptides
and polynucleotides are useful for inducing apoptosis, particularly when
apoptosis is p53-independent. They may be used to produce pharmaceutical
compositions which are used for treating a disease where enhanced cell
proliferation or decreased cell death is observed, particularly in cancer
or in autoimmune diseases, for diagnosing a disease related with

CC	aberrancies in the apoptotic process, and for detecting the presence of									
CC	cancer cells or cells that are prone to cancer									
XX										
SQ	Sequence	947 BP;	309 A;	238 C;	198 G;	198 T;	0 U;	4 Other;		
	Query Match	99.7%; Score 944.2; DB 4; Length 947;								
	Best Local Similarity	100.0%; Pred. No. 7.9e-250;								
	Matches	947;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	ACCANACCCAAAAAGAGATCTGGAAATTCGGATTCCTCGAGGCCACGAAAGGCCGAAACAG	60							
Qy	61	TGCTGAGCCTTTAAATGCAAGCATCTCGGATGTGAGGAAGGCACCTCCACCAAGAAACC	120							
Db	61	TGCTGAGCCTTTAAATGCAAGCATCTCGGATGTGAGGAAGGCACCTCCACCAAGAAACC	120							
Qy	121	TCGGATCAATTTCTCAGCTGGTGCNCAACAAAGTGGCACACATATGCCACCCACCACAC	180							
Db	121	TCGGATCAATTTCTCAGCTGGTGCNCAACAAAGTGGCACACATATGCCACCCACCACAC	180							
Qy	181	CCCTAAAGGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGA	240							
Db	181	CCCTAAAGGAGAGAGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGA	240							
Qy	241	CAAGGAATTTAGTCTCTAGTGTACCAAGAAATACCAACAGAAACCAACCAAGTTC	300							
Db	241	CAAGGAATTTAGTCTCTAGTGTACCAAGAAATACCAACAGAAACCAACCAAGTTC	300							
Qy	301	TGACATTTCTGAAAGATCTCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTACAAC	360							
Db	301	TGACATTTCTGAAAGATCTCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTACAAC	360							
Qy	361	AAAGACGAGCAACAAATCACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCAC	420							
Db	361	AAAGACGAGCAACAAATCACACCTCAAGGCCCGGCTGAAAAACGTGGACAGGAGCAC	420							
Qy	421	TGCACAGCAGTTGGCAGTAATCTGGGACAGCTCACCGTCATTATCACAGACTTTAAGGA	480							
Db	421	TGCACAGCAGTTGGCAGTAATCTGGGACAGCTCACCGTCATTATCACAGACTTTAAGGA	480							
Qy	481	AAAGACTCGCTCTCTATCGACATCTCTATCCACAGTGACCTCCAGTGCAGGGTCAGAAACA	540							
Db	481	AAAGACTCGCTCTCTATCGACATCTCTATCCACAGTGACCTCCAGTGCAGGGTCAGAAACA	540							
Qy	541	GCAGAACAGASACAGCTCGGGGTGAGAGACAAGAGGGCTCCTCCGCTTCCTCCAC	600							
Db	541	GCAGAACAGASACAGCTCGGGGTGAGAGACAAGAGGGCTCCTCCGCTTCCTCCAC	600							
Qy	601	GCCAAAGGGCGACATGTCAGCAGCTCAATGATGAATCTTTCTGAAATTTGCACATGGAAATG	660							
Db	601	GCCAAAGGGCGACATGTCAGCAGCTCAATGATGAATCTTTCTGAAATTTGCACATGGAAATG	660							
Qy	661	TGAAACATATGAATCAAGGATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTTGCATC	720							
Db	661	TGAAACATATGAATCAAGGATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTTGCATC	720							
Qy	721	CTTGAGAAATCTTCTGTGGACATCGACCTCTTATGATGATGTCGACGATTAATTTCTGCTT	780							
Db	721	CTTGAGAAATCTTCTGTGGACATCGACCTCTTATGATGATGTCGACGATTAATTTCTGCTT	780							
Qy	781	GCCATGGGCATCTGGCCACCAGGAATTTGCGACCTCGAGTACTCTTGACACTTTTA	840							
Db	781	GCCATGGGCATCTGGCCACCAGGAATTTGCGACCTCGAGTACTCTTGACACTTTTA	840							
Qy	841	TGTAATCCATTTGTTTATATGATTTTCTAAACATCATTTATTAATTTGGATGCTCCTCTGA	900							
Db	841	TGTAATCCATTTGTTTATATGATTTTCTAAACATCATTTATTAATTTGGATGCTCCTCTGA	900							
Qy	901	ATCTACTTTTTTATAAAAAAGCCTTGTGGCCTCGAGAGATCTATGA	947							
Db	901	ATCTACTTTTTTATAAAAAAGCCTTGTGGCCTCGAGAGATCTATGA	947							

RESULT 2	
AAF55404	
ID	AAF55404 standard; DNA; 947 BP.
XX	
AC	AAF55404;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	Nucleotide sequence of an apoptin-associating protein.
XX	
KW	Apoptin-associating proteinaceous substance; cell proliferation;
KW	apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW	autoimmune disease; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	54..95
CDS	
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FT	/note= "encodes AAB67552"
FT	96..311
FT	/*tag= b
FT	/transl_except= (pos: 144..146, aa: Xaa)
FT	/note= "Xaa is an unspecified residue; encodes AAB67553"
FT	312..401
FT	/*tag= c
FT	/note= "encodes AAB67554"
FT	402..440
FT	/*tag= d
FT	/note= "encodes AAB67555"
FT	441..518
FT	/*tag= e
FT	/note= "encodes AAB67556"
FT	519..884
FT	/*tag= f
FT	/transl_except= (pos: 552..554, aa: Xaa)
FT	/note= "Xaa is an unspecified residue; encodes AAB67557"
FT	885..920
FT	/*tag= g
FT	/note= "encodes AAB67558"
XX	
EP	1081226-A1.
PN	
XX	
PD	07-MAR-2001.
XX	
PF	02-SEP-1999; 99EP-00202858.
XX	
PR	02-SEP-1999; 99EP-00202858.
XX	
PA	(LEAD-) LEADD BV.
XX	
DR	WPI; 2001-219813/23.
DR	P-PSDB; AAB67552, AAB67553, AAB67554, AAB67555, AAB67556, AAB67557,
DR	AAB67558.
XX	
PT	Novel isolated or recombinant apoptin-associating proteinaceous
PT	substance, apoptin-associating protein 1, useful for inducing apoptosis
PT	for treating cancer or autoimmune diseases caused by aberrant apoptosis.
XX	
PS	Claim 4; Fig 1; 29pp; English.
XX	
CC	The present sequence encodes an apoptin-associating proteinaceous
CC	substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC	inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC	inducing a p53-independent apoptosis. They are used for treating a
CC	disease where enhanced proliferation or decreased cell death is observed
CC	e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC	diseases related with aberrations in the apoptotic process such as cancer
CC	and autoimmune diseases
XX	
SQ	Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;

QY 301 TGACATTCTGAAGATCCTCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTCAAC 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 TGACATTCTGAAGATCCTCTCTAGTGAAGCAACACAGCATACAGTCTGCAAAATGCTCAAC 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 AAAGACGAGGAAACAAATACACACTCAAGGCCCGGCTGAAACACGTGACAGGAGCAC 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 421 TGACAGAGTGGGAGTAATCTGTGGGCAACGTCACCGTCATTATACAGACTTTAAGGA 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 AAAGACTCGCTCCTCATCGCATCCTCATCCAGTGACCTCCAGTGACGGTCTGAGACA 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 GCAGAACGAGACGCTCGGGGTGAGAGACAGACAAGGGCTCCTCCGCTTCCCTCCAC 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 GCCAAGGGGACATGTCAGAGTCAATGATGAATCTTTCTGAAATGCGACATGGAATTG 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 TGAAAATATGATCAGGGTATGAAATCAAAACCTCCACCTGCCATGCTGCTTGCAATC 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 721 CCTGGAGAAATCTTCTGTGGACATCGACCTCTTATGATGCTGCCAGGATAATTTCTGCTT 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 GCGATGGGACATCTGGCCACCAAGGAATTTGCAACCTTGACAGATTAATCTTTGACACTTTTA 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 TGTAATCCATTTTATATATGATTTTCTTAACATCAATTTATATATTTGGATGCTCCTGTA 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 ATCTACTTTTTATAAAAAGCCCTTGTGGCCTCGAGAGATCTATGA 947
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAAF55596 standard; cDNA; 1131 BP.
AC AAF55596;
XX
XX 29-MAY-2001 (first entry)
DT Nucleotide sequence of apoptin-associating protein 1 cDNA clone b.
XX
DE Apoptin-associating protein; AAP; apoptosis; cell proliferation;
XX cell death; autoimmune disease; cancer; ss.
KW Homo sapiens.
XX
XX WO200116165-A2.
PN
XX
XX 08-MAR-2001.
PD
XX
XX 01-SEP-2000; 2000WO-NL000612.
XX
XX 02-SEP-1999; 99EP-00202858.
PR
XX 21-OCT-1999; 99EP-00203465.
XX
XX (LEAD-) LEADD BV.
PA
XX Noteborn MHM, Danen-Van Oorschot AAAM;
PI
XX

DR WPI; 2001-235090/24.
XX New nucleic acids encoding apoptin-associating proteins useful for
PT inducing apoptosis, particularly p53 independent apoptosis, or for
PT treating cancers or autoimmune diseases.
XX
PS Claim 6; Fig 2; 50pp; English.
XX
CC The present sequence encodes a human apoptin-associating protein 1
CC (AAP1). The protein is capable of providing apoptosis. AAP polypeptides
CC and polynucleotides are useful for inducing apoptosis, particularly when
CC apoptosis is p53-independent. They may be used to produce pharmaceutical
CC compositions which are used for treating a disease where enhanced cell
CC proliferation or decreased cell death is observed, particularly in cancer
CC or in autoimmune diseases, for diagnosing a disease related with
CC aberrancies in the apoptotic process, and for detecting the presence of
CC cancer cells or cells that are prone to cancer
XX
SQ Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
Query Match 93.2%; Score 883; DB 4; Length 1131;
Best Local Similarity 97.7%; Pred. No. 6.7e-233;
Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
QY 24 GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTCTGAAGCCTTTAAATGCAGCA 83
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 209 GGTITTTGGATTTGTAGCGTCTGCACCTTCAGAAACAGTGTGCTTAAATGCAGCA 268
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 84 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAAAACCTCGGATCAATTTCTAGCTGGTGG 143
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 269 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAAAACCTCGGATCAATTTCTAGCTGGTGG 328
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 144 CACAAAGTGTGCAACAAGATATGCCACCCACACCCCTAAAAAGGAGAAAGAGCA 203
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 329 CACAAAGTGTGCAACAAGATATGCCACCCACACCCCTAAAAAGGAGAAAGAGCA 388
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 204 AAGTTCAAAAGCAGGACAAAGAAACCTGAGAAAGCAAGGAAATTAGTCTAGTGTGA 263
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 389 AAGTTGAAAAGCAGGACAAAGAAACCTGAGAAAGCAAGGAAATTAGTCTAGTGTGA 448
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QY 264 CCAAGAAAAATACCAACAGAAAAACCAAAACCAAGTCTGACATTTCTGAAAGATCTCCTTA 323
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 449 CCAAGAAAAATACCAACAGAAAAACCAAAACCAAGTCTGACATTTCTGAAAGATCTCCTTA 508
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 324 GTGAACCAACAGCATACAGTCTGCAATGCTACCAACAGAACGACGGAACCAATCACA 383
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 509 GTGAACCAACAGCATACAGTCTGCAATGCTACCAACAGAACGACGGAACCAATCACA 568
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 384 CTTCAAGGCCCGGCTGAAAAACGTCGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTG 443
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QY 569 CTTCAAGGCCCGGCTGAAAAACGTCGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTG 628
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 444 TGGGCAACGTCACCGTCATTATCAGAGCTTTAAGGAAAAAGACTCGCTCTCTATGACAT 503
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QY 629 TGGGCAACGTCACCGTCATTATCAGAGCTTTAAGGAAAAAGACTCGCTCTCTATGACAT 688
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QY 504 CTTCAATCCACAGTGCCTCCAGTGCAGGCTGAGAACAGCAGACACAGACAGCTCGGGGT 563
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QY 689 CTTCAATCCACAGTGCCTCCAGTGCAGGCTGAGAACAGCAGACACAGACAGCTCGGGGT 748
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QY 564 CAGAGAGCAGACAAAGGGCTCCTCCCGTTCTCTCACCGCCAAAGGCGACATGTCAGCAG 623
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QY 749 CAGAGAGCAGACAAAGGGCTCCTCCCGTTCTCTCACCGCCAAAGGCGACATGTCAGCAG 808
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 624 TCAATGATGAATCTTTCTGAAATGTCATGGAATTTGTGAAAACTATGAAATCAGGGTATG 683
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 809 TCAATGATGAATCTTTCTGAAATGTCATGGAATTTGTGAAAACTATGAAATCAGGGTATG 868
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 684 AATTTCAAAACCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 869 AATTTCAAAACCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 928
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGGCATGCGCATCTGGCCACCAAG 803

Db 929 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 988
Qy 804 GAATTTGCGACCTCGAGCATCTCTTGACACTTTTATGTAATTCCTATGTTTATATGAT 863
Db 989 GAATTTGCGACCTCGAGCATCTCTTGACACTTTTATGTAATTCCTATGTTTATATGAT 1048
Qy 864 TTTCTCAACATCAATTTATATATGATGCTCTGGAATCTACTTTTATATAAAAAAGCC 923
Db 1049 TTTCTCAACATCAATTTATATATGATGCTCTGGAATCTACTTTTAT-AAAAAGGCC 1107
Qy 924 TTYGTGGCCTCGAGATCTATGA 947
Db 1108 TTGTTGGCCTCGAGATCTATGA 1131

RESULT 5
AAF55405
ID AAF55405 standard; DNA; 1131 BP.
XX AAF55405;
AC AAF55405;
DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of an apoptin-associating protein.
XX Apoptin-associating proteinaceous substance; cell proliferation;
KW apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW autoimmune disease; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..828
FT /*tag= a
FT /note= "encodes AAB67559"
FT CDS 829..939
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XX EP1081226-A1.
XX 07-MAR-2001.
XX 02-SEP-1999; 99EP-00202858.
XX 02-SEP-1999; 99EP-00202858.
XX (LEAD-) LEADD BV.
XX WPI; 2001-219813/23.
XX P-PSDB; AAB67559, AAB67560, AAB67561, AAB67562, AAB67563.
XX Novel isolated or recombinant apoptin-associating proteinaceous
PT substance, apoptin-associating protein 1, useful for inducing apoptosis
PT for treating cancer or autoimmune diseases caused by aberrant apoptosis.
XX Claim 4; Fig 2; 29pp; English.

XX The present sequence encodes an apoptin-associating proteinaceous
CC substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC inducing a p53-independent apoptosis. They are used for treating a
CC disease where enhanced proliferation or decreased cell death is observed

CC e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC diseases related with aberrations in the apoptotic process such as cancer
CC and autoimmune diseases
XX Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
SQ Query Match 93.2%; Score 883; DB 4; Length 1131;
Best Local Similarity 97.7%; Pred. No. 6.7e-233;
Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
Qy 24 GGAATTCGATCTCTCGAGGCGCGAAGGCGGAAACAGCTGCTGAAGCCTTTAAATGACGA 83
Db 209 GGTTTTGGGATTTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGACGA 268
Qy 84 TCTGCGATGTAGGAAAGGCACTCCACCCAGAAAACCTCGGATCAATTTCTCAGCTGTGG 143
Db 269 TCTGCGATGTAGGAAAGGCACTCCACCCAGAAAACCTCGGATCAATTTCTCAGCTGTGG 328
Qy 144 CNCAACAAGTGGCACAACAGATATGCCACCCACCCCTTAAAGAGGAGAGAGAGA 203
Db 329 CACAACAAGTGGCACAACAGATATGCCACCCACCCCTTAAAGAGGAGAGAGAGA 388
Qy 204 AAGTTGAAAGCAGGACAAGAGAAACCTCGAAGCAAGGAAATTTAGTCTAGTGTGA 263
Db 389 AAGTTGAAAGCAGGACAAGAGAAACCTCGAAGCAAGGAAATTTAGTCTAGTGTGA 448
Qy 264 CCAAGAAAATATCAACAAGAAAACCAACCAAGTCTGACATCTCTGAAAGATCCTCTA 323
Db 449 CCAAGAAAATATCAACAAGAAAACCAACCAAGTCTGACATCTCTGAAAGATCCTCTA 508
Qy 324 GTGAAGCAACAGCATACAGTCTGCAAAATGCTCAACAAGACGAGGCAAAACAAATCACA 383
Db 509 GTGAAGCAACAGCATACAGTCTGCAAAATGCTCAACAAGACGAGGCAAAACAAATCACA 568
Qy 384 CTTCAAGGCCCCGGCTGAAAACGTCGACAGGAGCACTGCACAGCAGTTCGCGACTACTG 443
Db 569 CTTCAAGGCCCCGGCTGAAAACGTCGACAGGAGCACTGCACAGCAGTTCGCGACTACTG 628
Qy 444 TGGGCAACGTCACCGTCATTATCAGACATTTTAAAGAAAAGACTCGCTCTCATCGACAT 503
Db 629 TGGGCAACGTCACCGTCATTATCAGACATTTTAAAGAAAAGACTCGCTCTCATCGACAT 688
Qy 504 CTTCAATCCACAGTACCTCCAGTGCAGGGTGCAGAACGAGAACCCAGACAGCTCGGGGT 563
Db 689 CTTCAATCCACAGTACCTCCAGTGCAGGGTGCAGAACGAGAACCCAGACAGCTCGGGGT 748
Qy 564 CAGAGACACAGACAGGAGGCTCTCCGCTTCTCCAGCCAGGAGGCGACATGTCAGCAG 623
Db 749 CAGAGACACAGACAGGAGGCTCTCCGCTTCTCCAGCCAGGAGGCGACATGTCAGCAG 808
Qy 624 TCAATGATGAATCTTTCTGAAATTTGCACATGGAATTTGAAAACATATGAATCAGGGGTATG 683
Db 809 TCAATGATGAATCTTTCTGAAATTTGCACATGGAATTTGAAAACATATGAATCAGGGGTATG 868
Qy 684 AAATTTCAAAACCTCCACCTCCATGCTGCTTGCATCCCTTGGAGAAATCTTCTGTGGACAT 743
Db 869 AAATTTCAAAACCTCCACCTCCATGCTGCTTGCATCCCTTGGAGAAATCTTCTGTGGACAT 928
Qy 744 CGACCTCTTAGTGATGCTGCAAGGATTAATTTCTGCTTGCATGCGGATCTGGCCACCAAG 803
Db 929 CGACCTCTTAGTGATGCTGCAAGGATTAATTTCTGCTTGCATGCGGATCTGGCCACCAAG 988
Qy 804 GAATTTGCGACCTCGAGCATCTCTTGACACTTTTATGTAATTCCTATGTTTATATGAT 863
Db 989 GAATTTGCGACCTCGAGCATCTCTTGACACTTTTATGTAATTCCTATGTTTATATGAT 1048
Qy 864 TTTCTCAACATCAATTTATATATGATGCTCTGGAATCTACTTTTATATAAAAAAGCC 923
Db 1049 TTTCTCAACATCAATTTATATATGATGCTCTGGAATCTACTTTTAT-AAAAAGGCC 1107
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Db 1108 TTYGTGGCCTCGAGATCTATGA 1131

RESULT 6	AAF57185	AAF57185 standard; cDNA; 1131 BP.
XX	AC	AAF57185;
XX	DT	29-MAY-2001 (first entry)
XX	DE	Apoptin-associating protein (AAP)-1-b nucleotide sequence.
XX	KW	Apoptin-associating protein; AAP; apoptosis; p53; cell proliferation;
KW	KW	cell death; cancer; autoimmune disease; cytostatic; immunosuppressive;
KW	KW	gene therapy; AAP-1-b; ss.
XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
XX	CDS	76..1131
FT	FT	/*tag= a
FT	FT	/transl_except= (pos:826..828, aa:Xaa)
FT	FT	/transl_except= (pos:937..939, aa:Xaa)
FT	FT	/transl_except= (pos:940..942, aa:Xaa)
FT	FT	/transl_except= (pos:1015..1017, aa:Xaa)
FT	FT	/transl_except= (pos:1045..1047, aa:Xaa)
FT	FT	/transl_except= (pos:1054..1056, aa:Xaa)
FT	FT	/product= "partial AAP-1-b protein"
FT	FT	/note= "Xaa are residues encoded by stop codons"
XX	PN	BP1083224-A2.
XX	XX	14-MAR-2001.
XX	XX	01-SEP-2000; 2000EP-00203042.
XX	XX	02-SEP-1999; 99EP-00202858.
PR	PR	21-OCT-1999; 99EP-00203465.
XX	XX	(LEAD-) LEADD BV.
XX	PA	Noteborn MMH, Danen-Van Oorschot AAM;
XX	PI	WPI; 2001-228257/24.
DR	DR	P-PSDB; AAB62059.
XX	XX	New nucleic acids encoding apoptin-associating proteins capable of
PT	PT	inducing p52 independent apoptosis, useful for treating a disease
PT	PT	associated with enhanced cell proliferation or decreased cell death, e.g.
PT	PT	cancer or autoimmune disease.
XX	XX	Claim 6; Fig 2; 26pp; English.
XX	XX	The invention provides isolated or recombinant nucleic acid (I), its
CC	CC	functional encoding an apoptin-associating proteinaceous (AAP) substance
CC	CC	capable of apoptosis. (I), the vector comprising (i), the host cell
CC	CC	comprising the vector and the proteinaceous substance encoded by (i) are
CC	CC	useful for inducing apoptosis, particularly p53-independent apoptosis,
CC	CC	and for treating a disease where enhanced cell proliferation or decreased
CC	CC	cell death is observed, such as cancer or an autoimmune disease. A
CC	CC	composition comprising the nucleic acid or the AAP may further be used
CC	CC	for diagnosing a disease related with aberrancies in the apoptotic
CC	CC	process, and for detecting the presence of cancer cells or cells that are
CC	CC	prone to cancer. The present sequence represents the nucleotide sequence
CC	CC	of the AAP-1-b cDNA clone encoding a partial AAP-1-b protein
XX	SQ	Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
XX	XX	Query Match 93.2%; Score 883; DB 5; Length 1131;
XX	XX	Best Local Similarity 97.7%; Pred. No. 6.7e-233;
XX	XX	Matches 903; Conservative 2; Mismatches 18; Indels 1; Gaps 1;
XX	XX	24 GGAATTCCGATCCTCGAGGCCACGAGGCCGAAACAGTGTGGAAGCCCTTTAAATGCAGCA 83

XX	Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW	antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;
KW	gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
KW	diabetic retinopathy; cardiovascular disease; atherosclerosis;
KW	ischemic limb disease; coronary artery disease; gene; ds.
XX	
OS	Homo sapiens.
PN	WO2003027285-A1.
XX	
PD	03-APR-2003.
XX	
PF	19-SEP-2002; 2002WO-AU001282.
XX	
PR	27-SEP-2001; 2001AU-00007973.
PR	27-SEP-2001; 2001AU-00007974.
PR	11-OCT-2001; 2001AU-00008210.
PR	29-OCT-2001; 2001AU-00008532.
PR	13-NOV-2001; 2001AU-00008838.
PR	28-AUG-2002; 2002AU-00951032.
XX	
PA	(BION-) BIONOMICS LTD.
PI	Gamble JR, Hahn CN, Vadas MA;
XX	
DR	WPI; 2003-354655/33.
DR	P-PSDB; ABR64205.
XX	
PT	New angiogenic genes and polypeptides, useful for diagnosing,
PT	prognosticating or treating an angiogenesis-related disorder, e.g.
PT	cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
PT	cardiovascular diseases.
XX	
PS	Claim 2; SEQ ID NO 35; 90pp; English.
XX	
CC	The invention relates to the isolation of novel genes (ACF34446-ACF34559)
CC	encoding proteins (ABR64281) involved in the process of
CC	angiogenesis. The nucleic acid molecules are useful in identifying and/or
CC	obtaining full-length human genes involved in an angiogenic process. The
CC	nucleic acid molecule, polypeptides or complexes encoded, cells or
CC	genetically modified non-human animals derived from these are useful for
CC	the screening of candidate pharmaceutical compounds used in treating
CC	angiogenesis-related disorders. They are also useful for diagnosing,
CC	prognosticating or treating an angiogenesis-related disorder, which
CC	involves uncontrolled or enhanced angiogenesis or is a disorder in which
CC	a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
CC	diabetic retinopathy, psoriasis or cardiovascular diseases such as
CC	atherosclerosis), or involves inappropriately arrested or decreased
CC	angiogenesis or is a disorder in which an expanding vasculature is of
CC	benefit (e.g. ischemic limb disease or coronary artery disease). The
CC	modulator of expression or activity of the polypeptide encoded by the
CC	nucleic acid sequence is useful for manufacturing a medicament for the
CC	treatment of an angiogenesis-related disorder. This sequence corresponds
CC	to the gene encoding one of the novel angiogenic protein
XX	
SQ	Sequence 1128 BP; 341 A; 290 C; 282 G; 215 T; 0 U; 0 Other;
Query Match 91.9%; Score 870; DB 8; Length 1128;	
Best Local Similarity 98.0%; Pred. No. 2.6e-229;	
Matches 879; Conservative 1; Mismatches 17; Indels 0; Gaps 0	
QY	24 GGAATTCCGGATCTCTGAGGCCACGAAGCGCGAAACAGTGTGAAGCCTTTAAATGCAGCA 83
DB	219 GGTTTTGGGATGTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCAGCA 278
QY	84 TCTGCGATGTGAGAAAGGCACCTCCACGAGAAAACCTTCGGATCAATTCTCAGCTGTGG 143
DB	279 TCTGCGATGTGAGAAAGGCACCTCCACGAGAAAACCTTCGGATCAATTCTCAGCTGTGG 338
QY	144 CNCAACAAGTGGCAACAAGTATGCAACCCCAACACCCCTTAAAGAGAGAGAGAGA 203
DB	339 CGCAACAAGTGGCAACAAGTATGCAACCCCAACACCCCTTAAAGAGAGAGAGAGA 398

CC The invention relates to an inhibitory RNA (RNAi) molecule derived from a
CC nucleic acid molecule comprising a defined nucleic acid sequences given
CC in the specification or a sequence which hybridizes to the sequences and
CC encodes a Notch signaling target gene or which is a degenerate as a
CC result of the genetic code of the sequences. The methods and compositions
CC of the present invention are useful for manipulating the phenotype of
CC stem cells, preferably pluripotent stem cells. This sequence corresponds
CC to one of the nucleic acid molecules of the invention.
XX
XX
SQ

Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 91.7%; Score 868.4; DB 10; Length 1036;
Best Local Similarity 97.9%; Pred. No. 6.8e-229;
Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Qy 24 GGAATTCGGATCTCTGAGGCCACGAGCCGAAACGCTGCTGAAGCCCTTTAAATGCAGCA 83
Db 135 GGTTTGGGATTTAGCGTCTGCACTTCAAGAACAGTGTGAAGCCCTTTAAATGCAGCA 194
Qy 84 TCTCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 143
Db 195 TCTCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 254
Qy 144 CNCAACAGTGGCAACAGTATGCCCCACCAACCCCTTAAAGAGGAGGAAGGAGA 203
Db 255 CACAACAGTGGCAACAGTATGCCCCACCAACCCCTTAAAGAGGAGGAAGGAGA 314
Qy 204 AAGTTGAAAGCAGGACAAAGAGAACTGTGAGAAAGCAAGGAATTTAGTCTAGTGTGA 263
Db 315 AAGTTGAAAGCAGGACAAAGAGAACTGTGAGAAAGCAAGGAATTTAGTCTAGTGTGA 374
Qy 264 CCAAGAAATATACCAAGAAAGAAACCAAACTGACATCTGAAAGATCTCTCTA 323
Db 375 CCAAGAAATATACCAAGAAAGAAACCAAACTGACATCTGAAAGATCTCTCTA 434
Qy 324 GTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGAACCCAGCGGAAACAAATCACA 383
Db 435 GTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGAACCCAGCGGAAACAAATCACA 494
Qy 384 CCTAAGCCCGGCTGAAAAACGTGGACAGGACCTGCAAGAGTGGTGGCAGTACTG 443
Db 495 CCTAAGCCCGGCTGAAAAACGTGGACAGGACCTGCAAGAGTGGTGGCAGTACTG 554
Qy 444 TGGGCAAGCTCACCGTCTATTCACAGACTTTAAGGAAAGACTCGCTCTCATCGACAT 503
Db 555 TGGGCAAGCTCACCGTCTATTCACAGACTTTAAGGAAAGACTCGCTCTCATCGACAT 614
Qy 504 CCTCATCCACAGTGAACCTCCAGTGCAGGGTTCAGAACAGACAGACAGTCTGGGGT 563
Db 615 CCTCATCCACAGTGAACCTCCAGTGCAGGGTTCAGAACAGACAGACAGTCTGGGGT 674
Qy 564 CAGAGACACAGCAAGGGCTCTCCCGTTCTCCAGCCCAAGGGCGACATGTCAGCAG 623
Db 675 CAGAGACACAGCAAGGGCTCTCCCGTTCTCCAGCCCAAGGGCGACATGTCAGCAG 734
Qy 624 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACCTATCAATCAGGATG 683
Db 735 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGAAACCTATCAATCAGGATG 794
Qy 684 AAATTCAAAACCTCCACCTGCCCCTGCTGTCATCCCTGGAGAACTCTCTGTGGACAT 743
Db 795 AAATTCAAAACCTCCACCTGCCCCTGCTGTCATCCCTGGAGAACTCTCTGTGGACAT 854
Qy 744 CGACCTCTTAGTATGCTGCGAGGATTAATTTCTGCTGGCATGCGGCACCCAG 803
Db 855 CGACCTCTTAGTATGCTGCGAGGATTAATTTCTGCTGGCATGCGGCACCCAG 914
Qy 804 GAAATTCGACCCCTGACGATTTACTCTTGACACTTTTATGTTTATATATCAT 863
Db 915 GAAATTCGACCCCTGACGATTTACTCTTGACACTTTTATGTTTATATATCAT 974
Qy 864 TTTCTCAACATCATTTAATTTGATGTGCTCTCTGAATCTACTTTTATAAAAA 920

Db 975 TTTCCTAACAAATCATTTATAATTTGGATGTGCTCCTGAACTACTTTTATAAAAAA 1031

RESULT 10

ADK61399
ID ADK61399 standard; DNA; 1036 BP.

XX AC ADK61399;

XX 06-MAY-2004 (first entry)

XX Ovarian cancer-related DNA #554 with altered ovarian cancer expression.

XX ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

XX gene expression; primer; cancer.

XX Homo sapiens.

XX WO2003068054-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-US004688.

XX 13-FEB-2002; 2002US-0357031P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Jazaeri AA, Boyd J, Liu ET;

XX WPI; 2003-689589/65.

XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
XX like tumor by determining a pattern of expression in the ovarian tumor of
XX several markers.

XX Disclosure; SEQ ID NO 569; 137pp; English.

XX The invention relates to a method of classifying an ovarian tumor as a
XX BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
XX pattern of expression in the ovarian tumor of several markers given in
XX the specification; and (2) comparing a similarity of the pattern of
XX expression of the markers in the ovarian tumor to a pattern of expression
XX of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
XX like or non-BRCA-like tumor. The method is useful for classifying an
XX ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
XX This sequence corresponds to an ovarian cancer -related gene having an
XX altered pattern of expression in ovarian cancer. (Note: The sequence data
XX for this patent did not form part of the printed specification but was
XX obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences).

XX SQ Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 91.7%; Score 868.4; DB 10; Length 1036;

Best Local Similarity 97.9%; Pred. No. 6.8e-229;

Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Qy 24 GGAATTCGGATCTCTGAGGCCACGAGCCGAAACAGTGTGAAGCCCTTTAAATGCAGCA 83

Db 135 GGTTTGGGATTTAGCGTCTGCACTTCAAGAACAGTGTGAAGCCCTTTAAATGCAGCA 194

Qy 84 TCTCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 143

Db 195 TCTCGATGTGAGGAAGGACCTCCACGAGAAACCTCGGATCAATTTCTCAGCTGGTGG 254

Qy 144 CNCAACAGTGGCAACAGTATGCCACCCCAACCCCTTAAAGAGGAGGAAGGAGA 203

Db 255 CACAACAGTGGCAACAGTATGCCACCCCAACCCCTTAAAGAGGAGGAAGGAGA 314

Qy 204 AAGTTGAAAGCAGGACAAAGAGAACTGTGAGAAAGCAAGGAAATTTAGTCTAGTGTGA 263

Db 315 AAGTTGAAGCAGGCAAGAGAGAACTCTGAGAAGCAAGGAAATTTAGTCCTAGTGTTA 374
Qy 264 CCAAGAAAAATATCCAAAGAAAAACCAAAACCAAGTCTGACATTTCTGAAAGATCCTCCTA 323
Db 375 CCAAGAAAAATATCCAAAGAAAAACCAAAACCAAGTCTGACATTTCTGAAAGATCCTCCTA 434
Qy 324 GTGAAGCAACAGCATACAGTCTCAATCTCAACCAAGACCCAGCGAAACCAATCACA 383
Db 435 GTGAAGCAACAGCATACAGTCTCAATCTCAACCAAGACCCAGCGAAACCAATCACA 494
Qy 384 CCTCAAGCCCGGCTGAAAAACCTGGACAGGACACTGCACAGCAGTTCGGCACTAAGT 443
Db 495 CCTCAAGCCCGGCTGAAAAACCTGGACAGGACACTGCACAGCAGTTCGGCACTAAGT 554
Qy 444 TGGGCAACGTCACCGTCATTATCAAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT 503
Db 555 TGGGCAACGTCACCGTCATTATCAAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT 614
Qy 504 CCTCATCCACAGTCACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGCAGCTCGGGGT 563
Db 615 CCTCATCCACAGTCACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGCAGCTCGGGGT 674
Qy 564 CAGAGACACAGACAAGGGCTCTCCCGTCTCCAGCCGCAAGGGGCGACATGTCAGCAG 623
Db 675 CAGAGACACAGACAAGGGCTCTCCCGTCTCCAGCCGCAAGGGGCGACATGTCAGCAG 734
Qy 624 TCAATGATGAATCTTCTGAAATTCGACATGGAATTTGTAAGTATGAATCAGGGTATG 683
Db 735 TCAATGATGAATCTTCTGAAATTCGACATGGAATTTGTAAGTATGAATCAGGGTATG 794
Qy 684 AAATTTCAAAACCTCCAGCTCCCATGCTGCTGTCATCCCTGGAGAACTTCTGTCGACAT 743
Db 795 AAATTTCAAAACCTCCAGCTCCCATGCTGCTGTCATCCCTGGAGAACTTCTGTCGACAT 854
Qy 744 CGACCTCTTAGTGATGCTGCAGAGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 803
Db 855 CGACCTCTTAGTGATGCTGCAGAGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 914
Qy 804 GAATTTGGCAACCTTGACGATTAATCTTTGACACTTTTATGATTCATTTGTTTATATGAT 863
Db 915 GAATTTGGCAACCTTGACGATTAATCTTTGACACTTTTATGATTCATTTGTTTATATGAT 974
Qy 864 TTTCTTAACATCATTTTATATTAATTTGATGCTGCTCTGATCTACTTTTATAAAAAA 920
Db 975 TTTCTTAACATCATTTTATATTAATTTGATGCTGCTCTGATCTACTTTTATAAAAAA 1031

RESULT 11
ADD18793
ID ADD18793 standard; DNA; 4700 BP.
XX AC ADD18793;
XX AC
XX AC
DT 15-JAN-2004 (first entry)
XX DE Human disease related protein DNA sequence SeqID224.
XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemia; condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing; gene; ds.
XX OS Homo sapiens.
XX FN WO2003018621-A2.
XX PD 06-MAR-2003.
XX PF 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.
PR 05-OCT-2001; 2001GB-00024037.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX WPI; 2003-290046/28.
XX P-PSDB; ADD18792.
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX Claim 27; SEQ ID NO 224; 424pp; English.
PS This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory, the
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
SQ Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;
Query Match 91.5%; Score 866.8; DB 10; Length 4700;
Best Local Similarity 97.8%; Pred. No. 3.9e-228;
Matches 877; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
Qy 24 GGAATTCGGATCTCGAGGCCAGGAAGGCGGAAACAGTGTCTGAAGCCTTTAAATGACGA 83
Db 260 GGTGTTGGGATTTAGCGTCTGCACCTTCAGAAAACAGTGTCTGAAGCCTTTAAATGACGA 319
Qy 84 TCTGCCATGTGAGGAAGGCACCTCCACAGAAAACCTCGATCAATTTCTCAGCTGTGTG 143
Db 320 TCTGCCATGTGAGGAAGGCACCTCCACAGAAAACCTCGATCAATTTCTCAGCTGTGTG 379
Qy 144 CNCAACAAGTGGCAACACAGTATGCCACCCCTTAAACAGGAGGAAGAGGA 203
Db 380 CACAACAAGTGGCAACACAGTATGCCACCCCTTAAACAGGAGGAAGAGGA 439
Qy 204 AGTTGAAAGCAGGACAAAGAAACCTTGAGAAAGAACAGGAATTAGTCTTAGTGTTA 263
Db 440 AAGTTGAAAGCAGGACAAAGAAACCTTGAGAAAGAACAGGAATTAGTCTTAGTGTTA 499
Qy 264 CCAAGAAAATACCAACAGAAAACCAACCCAAAGTCTGACATTTCTGAAAGATCCTCCTA 323
Db 500 CCAAGAAAATACCAACAGAAAACCAACCCAAAGTCTGACATTTCTGAAAGATCCTCCTA 559
Qy 324 GTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCCAGCGAAACCAATCACA 383
Db 560 GTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCCAGCGAAACCAATCACA 619
Qy 384 CCTCAAGCCCGGCTGAAAAACCTGGACAGGACACTGCACAGCAGTTCGGCACTAAGT 443
Db 620 CCTCAAGCCCGGCTGAAAAACCTGGACAGGACACTGCACAGCAGTTCGGCACTAAGT 679
Qy 444 TGGGCAACGTCACCGTCATTATCAAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT 503
Db 680 TGGGCAACGTCACCGTCATTATCAAGACTTTAAGGAAAAAGACTCGCTCCTCATCGACAT 739
Qy 504 CCTCATCCACAGTCACCTCCAGTGCAGGGTTCAGAACAGCAGGACCTCGGGGT 563

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Db 740 CCTCATCCACAGTGAACCTCCAGTGCAGGGTCCGAACAGCAGAACCCAGCAGCTCGGGT 799
Qy 564 CAGAGACACAGCAAGGGCTCCCTCCGTTCTCCAGCGCCAAAGGGCGACATGTCAGCAG 623
Db 800 CTGAGACACAGCAAGGGCTCCCTCCGTTCTCCAGCGCCAAAGGGCGACATGTCAGCAG 859
Qy 624 TCAATGATGAATCTTCTGAAATTCACATGGAATTCGAAACTATGAATCAAGGATG 683
Db 860 TCAATGATGAATCTTCTGAAATTCACATGGAATTCGAAACTATGAATCAAGGATG 919
Qy 684 AAATTCAAAACCTCCACCTGCCCATGCTGTGATCCCTGGAGAAATCTTCTGTGGACAT 743
Db 920 AAATTCAAAACCTCCACCTGCCCATGCTGTGATCCCTGGAGAAATCTTCTGTGGACAT 979
Qy 744 CGACCTCTTAGTGTGCTGCAGATTAATCTGCTTGCATGGCATCTGGCCACCAAG 803
Db 980 CGACCTCTTAGTGTGCTGCAGATTAATCTGCTTGCATGGCATCTGGCCACCAAG 1039
Qy 804 GAATTCGCACCCCTGACGATTACTCTTGACACTTTTATGTTATTCATTTTATATGAT 863
Db 1040 GAATTCGCACCCCTGACGATTACTCTTGACACTTTTATGTTATTCATTTTATATGAT 1099
Qy 864 TTTCCTAACATCAATTTATTAATTCGATGTGCTCTGAAATCTACTTTTATAAAAAA 920
Db 1100 TTTCCTAACATCAATTTATTAATTCGATGTGCTCTGAAATCTACTTTTATAAAAAA 1156

RESULT 12
AAS34877
ID AAS34877 standard; cDNA; 2156 BP.
XX
AC AAS34877;
XX
DT 04-DEC-2001 (first entry)
XX
XX cDNA encoding novel human neoplastic disease associated polypeptide #111.
XX
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX
OS Homo sapiens.
XX
XX WO200155163-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001358.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
XX
XX 24-FEB-2000; 2000US-0184664P.
XX
XX 02-MAR-2000; 2000US-0186350P.
XX
XX 16-MAR-2000; 2000US-0189874P.
XX
XX 17-MAR-2000; 2000US-0190076P.
XX
XX 18-APR-2000; 2000US-0198123P.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX 28-JUN-2000; 2000US-0214886P.
XX
XX 30-JUN-2000; 2000US-0215135P.
XX
XX 07-JUL-2000; 2000US-0216647P.
XX
XX 07-JUL-2000; 2000US-0216880P.
XX
XX 11-JUL-2000; 2000US-0217487P.
XX
XX 14-JUL-2000; 2000US-0217496P.
XX
XX 26-JUL-2000; 2000US-0218290P.
XX
XX 26-JUL-2000; 2000US-0220963P.
XX
XX 14-AUG-2000; 2000US-0224518P.
XX
XX 14-AUG-2000; 2000US-0224519P.
XX
XX 14-AUG-2000; 2000US-0225213P.
XX
XX 14-AUG-2000; 2000US-0225214P.
XX
XX 14-AUG-2000; 2000US-0225266P.
XX
XX 14-AUG-2000; 2000US-0225267P.
XX
XX 14-AUG-2000; 2000US-0225268P.
XX
XX 14-AUG-2000; 2000US-0225270P.
XX
XX 14-AUG-2000; 2000US-0225447P.
XX
XX 14-AUG-2000; 2000US-0225757P.
XX
XX 14-AUG-2000; 2000US-0225758P.
XX
XX 14-AUG-2000; 2000US-0225759P.
XX
XX 18-AUG-2000; 2000US-0226791P.
XX
XX 22-AUG-2000; 2000US-0226681P.
XX
XX 22-AUG-2000; 2000US-0226868P.
XX
XX 22-AUG-2000; 2000US-0227182P.
XX
XX 23-AUG-2000; 2000US-0227009P.
XX
XX 30-AUG-2000; 2000US-0228924P.
XX
XX 01-SEP-2000; 2000US-0229287P.
XX
XX 01-SEP-2000; 2000US-0229343P.
XX
XX 01-SEP-2000; 2000US-0229344P.
XX
XX 01-SEP-2000; 2000US-0229345P.
XX
XX 05-SEP-2000; 2000US-0229509P.
XX
XX 06-SEP-2000; 2000US-0230437P.
XX
XX 06-SEP-2000; 2000US-0230438P.
XX
XX 08-SEP-2000; 2000US-0231242P.
XX
XX 08-SEP-2000; 2000US-0231243P.
XX
XX 08-SEP-2000; 2000US-0231244P.
XX
XX 08-SEP-2000; 2000US-0231413P.
XX
XX 08-SEP-2000; 2000US-0231414P.
XX
XX 08-SEP-2000; 2000US-0232080P.
XX
XX 08-SEP-2000; 2000US-0232081P.
XX
XX 12-SEP-2000; 2000US-0231968P.
XX
XX 14-SEP-2000; 2000US-0232397P.
XX
XX 14-SEP-2000; 2000US-0232398P.
XX
XX 14-SEP-2000; 2000US-0232399P.
XX
XX 14-SEP-2000; 2000US-0232400P.
XX
XX 14-SEP-2000; 2000US-0232401P.
XX
XX 14-SEP-2000; 2000US-0233063P.
XX
XX 14-SEP-2000; 2000US-0233064P.
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XX 14-SEP-2000; 2000US-0233065P.
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XX 21-SEP-2000; 2000US-0234223P.
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XX 21-SEP-2000; 2000US-0234274P.
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XX 23-SEP-2000; 2000US-0234997P.
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XX 25-SEP-2000; 2000US-0234998P.
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XX 26-SEP-2000; 2000US-0235484P.
XX
XX 27-SEP-2000; 2000US-0235834P.
XX
XX 27-SEP-2000; 2000US-0235836P.
XX
XX 29-SEP-2000; 2000US-0236327P.
XX
XX 29-SEP-2000; 2000US-0236367P.
XX
XX 29-SEP-2000; 2000US-0236368P.
XX
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PR 05-JAN-2001; 2001US-02559678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465558/50.
XX P-PSDB; AAU21678.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
XX diagnose diseases or disorders associated with aberrant expression or
XX activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
XX Claim 4; SEQ ID NO 121; 687pp; English.
XX
XX The present invention relates to the isolation of novel human neoplastic
XX disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
XX sequences encoding for these polypeptides. The sequences of the invention
XX are useful in the diagnosis, treatment, prevention and/or prognosis of
XX disorders involving neoplastic disease such as hyperproliferative
XX disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
XX glioma, adult liver cancer, childhood cerebellar astrocytoma, or
XX Hodgkin's lymphoma). The sequences of the invention may also be useful
XX for treating other disorders such as neural disorders, immune system
XX disorders, muscular disorders, reproductive disorders, gastrointestinal
XX disorders, pulmonary disorders, cardiovascular disorders and renal
XX disorders. The polynucleotide sequences of the invention are also useful
XX in gene therapy. AAS35050 represent cDNA sequences encoding for
XX the novel human neoplastic disease associated polypeptides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

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XX AC
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DT 18-DEC-2003 (first entry)
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KW Neoplastic disease-associated polypeptide; gene therapy;
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; hemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human; ss.
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 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-786918/74.
 DR P-PSDB; ADC46319.
 XX
 PT New isolated human neoplastic disease-associated polypeptides and
 PT polynucleotides, useful for diagnosing, preventing, prognosticating or
 PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
 PT disease.
 PT
 PS Claim 1; SEQ ID NO 121; 302pp; English.
 XX
 CC The invention relates to one of 238 disclosed human neoplastic disease-
 CC associated polypeptides encoded by 171 disclosed cDNA sequences
 CC (including their domains, epitopes, full-length proteins, allelic variants
 CC or species homologues). Also included are there encoding nucleic acids, a
 CC recombinant vector comprising the nucleic acid, a recombinant host cell
 CC comprising the nucleic acid (expressing the protein), an isolated
 CC antibody that binds specifically to the isolated polypeptide, preventing,
 CC treating or ameliorating a medical condition, diagnosing a pathological
 CC condition or a susceptibility to a pathological condition in a subject,
 CC identifying a binding partner to the polypeptide, identifying an activity
 CC in a biological assay, and the gene corresponding to the cDNA sequence.
 CC The polypeptides, polynucleotides and antibodies are useful for
 CC detecting, preventing, diagnosing, prognosticating, treating or
 CC ameliorating medical conditions such as hyperproliferative diseases or
 CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
 CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
 CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
 CC anaemia or thrombocytopaenia), allergic reactions including asthma or
 CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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 KW genome mapping; biodiversity; genetic disorder.
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 PD 17-APR-2003.
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10	42	4.4	260	2	US-08-897-126-29
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12	41.2	4.4	891	4	US-09-248-796A-11247
13	40.6	4.3	704	1	US-08-463-115-29
14	40.6	4.3	704	1	US-08-465-388-29
15	40.6	4.3	894	2	US-08-467-963C-28
16	40.6	4.3	894	2	US-08-838-189D-28
17	40.6	4.3	894	3	US-08-852-344D-28
18	40.6	4.3	894	3	US-08-344-639E-28
19	40.6	4.3	920	2	US-08-467-963C-7
20	40.6	4.3	920	2	US-08-838-189D-7
21	40.6	4.3	920	3	US-08-852-344D-7
22	40.6	4.3	920	3	US-08-344-639E-7
23	40.6	4.3	920	3	US-08-467-969A-7
24	40.6	4.3	920	3	US-08-467-961A-7
25	40.6	4.3	920	3	US-08-001-554A-7
26	40.6	4.3	2223	1	US-08-257-073-4
27	40.4	4.3	254964	4	US-09-949-016-12583

ALIGNMENTS

RESULT 1

US-09-513-999C-3095
Sequence 3095, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59 US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 3095

LENGTH: 376

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 69..374

FEATURE:

NAME/KEY: misc_feature

LOCATION: 367

OTHER INFORMATION: m=a or c

FEATURE:

NAME/KEY: UNSURE

LOCATION: 100

OTHER INFORMATION: Xaa=Lys or Thr

US-09-513-999C-3095

Query Match 9.9% Score 93.4; DB 4; Length 376;

Best Local Similarity 61.7%; Pred. No. 3.4e-19;

Matches 148; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy	27	ATTCGGATCTTCGAGGCCGGAAGCGCGAAGCCTTGAAGCCCTTTAAATGCAGCATCT	86
Db	133	ACTGGGACTGTAGGCTCTGCACCTTCGGAACGCGCGAGGCTTCAAGTGCATGATGT	192
Qy	87	GCAGTGTGAGAAAGGCACCTCCACGAAACCTCGATCAATTCCTCAGTGTGTCNC	146
Db	193	GCAGTGTGCGAAGGCGACCTCCACCGGAAACCTCGATCTCCAGTTGTTGCAC	252
Qy	147	AACAAGTGGCACACAGTATGCCACCCCTTAAAGGAGAGAGAGAGAAAG	206
Db	253	AGCAGGTTCACAGCTTTGTGCTCTCACAGTCAAGAAAGAGAAAGATTAAG	312

C	28	40.4	4.3	254964	4	US-09-949-016-17392	Sequence 17392, A
C	29	40.2	4.2	42000	4	US-10-081-563-25	Sequence 25, Appl
C	30	40.2	4.2	110585	4	US-09-949-016-13427	Sequence 13427, A
C	31	40.2	4.2	392000	4	US-10-027-983-11	Sequence 11, Appl
C	32	40	4.2	231	3	US-09-012-515A-20	Sequence 20, Appl
C	33	40	4.2	231	3	US-08-360-144A-20	Sequence 20, Appl
C	34	40	4.2	231	3	US-09-012-504A-20	Sequence 20, Appl
C	35	40	4.2	231	3	US-09-012-399A-20	Sequence 20, Appl
C	36	40	4.2	231	5	PCT-US95-06722-20	Sequence 24, Appl
C	37	40	4.2	826	2	US-08-408-095-24	Sequence 8, Appl
C	38	39.8	4.2	370	2	US-08-332-766A-8	Sequence 2801, Ap
C	39	39.6	4.2	2001	4	US-09-949-016-2801	Sequence 13042, A
C	40	39.6	4.2	150394	4	US-09-949-016-13042	Sequence 8976, Ap
C	41	39.4	4.2	399	4	US-09-621-976-8976	Sequence 12096, A
C	42	39.4	4.2	19566	4	US-09-949-016-12096	Sequence 14114, A
C	43	39.4	4.2	19567	4	US-09-949-016-14114	Sequence 16027, A
C	44	39.4	4.2	95109	4	US-09-949-016-16027	Sequence 19, Appl
C	45	39.2	4.1	3025	4	US-09-917-254-19	

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QY 207 TTGAAAAGCAGCAAAAGAGAACCTGAGAAAGACAGGAAATTTAGTCTAGTGTACCA 266
Db 313 TAGAAAAAGAAAAAGTGAAGAAAGGAAACAACTAGCAAAAAGAAATAGCCATAAGAMAACCA 372

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14

Query Match 6.1%; Score 57.6; DB 1; Length 7218;
Best Local Similarity 1.6%; Pred. No. 66/07;
Matches 6; Conservative 227; Mismatches 142; Indels 0; Gaps 0;

QY 9 CAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAACAGTCTGAAG 68
Db 1435 CRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1376

QY 69 CCTTTAAATCAGCATCTCGATGTGAGAAAGCACCTCCACAGAAAACCTCGGATCA 128
Db 1375 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316

QY 129 ATTCTAGCTGGTGCNCACAACTGCGACCAACAGTATGCCACCCACCCCTAAAA 188
Db 1315 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1256

QY 189 AGGAGAAGAGGAGAAAGTTCAAAGCAGCAAGCAAGAAACCTCGAGAAAGCAAGAAA 248
Db 1255 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1196
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QY 249 TTAGTCTCTAGTGTACCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTC 308
Db 1195 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1136

QY 309 TGAAGATCTCTCTAGTGAAGCAAAACAGCATACAGTCTCAAAATGCTACAAACAGCA 368
Db 1135 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1076

QY 369 GCGAAACAAATACCA 383
Db 1075 RRRRRRRRATCGCA 1061

RESULT 3
US-09-269-617-11
; Sequence 11, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,617
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1039 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE: Human cDNA library
; CLONE: SZ29
US-09-269-617-11

Query Match 5.8%; Score 54.8; DB 3; Length 1039;
Best Local Similarity 88.1%; Pred. No. 1.3e-06;
Matches 59; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAACAG 60
Db 53 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCGCAATC 112

QY 61 TGCTGAA 67
Db 113 TGAAGCA 119

RESULT 4
US-08-318-947A-1
; Sequence 1, Application US/08318947A
; Patent No. 5798245
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
```

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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
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; US-08-318-947A-1
;
; Query Match 5.6%; Score 53; DB 1; Length 1206;
; Best Local Similarity 98.1%; Pred. No. 5.4e-06;
; Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; Db 3 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 56
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; RESULT 5
; US-08-795-303-1
; Sequence 1, Application US/08795303
; Patent No. 5948656
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sughrue, Mion, Zimm, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/318,947
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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
;
; US-08-318-947A-1
;
; Query Match 5.6%; Score 53; DB 1; Length 1206;
; Best Local Similarity 98.1%; Pred. No. 5.4e-06;
; Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; Qy 1 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 54
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; RESULT 6
; US-09-269-617-13
; Sequence 13, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; CURRENT APPLICATION DATA:
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; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE:
; LIBRARY: Human cDNA library
; CLONE: SZ33
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; US-09-269-617-13
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; Query Match 5.5%; Score 52; DB 3; Length 1025;
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; Db 66 ACCAACCACCAAAAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGGCCG 119
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US-08-467-963C-28
; Sequence 28: Application US/08467963C
; Patent No. 5968776
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EMASYSYN, Mary E
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/467,963C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,189
; FILING DATE: 16-APR-1997
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-467-963C-28

Query Match 4.3%; Score 40.6; DB 2; Length 894;
Best Local Similarity 50.8%; Pred. No. 0.039;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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Qy 358 AACAAAGACCGGAAACAAATCACCTCAAGGCCCGGCTGAAAAACGTGGACAGG 417
Db 702 AACCATCAACCAACCAACCAACCAATCACACTACTGTCTCACCACACACACAGG 761
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Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	859	90.7	2156	14	US-10-103-313-121
6	469.6	49.6	502	10	US-09-918-995-24859
7	428.6	45.3	429	9	US-09-864-761-4575

8	357.4	37.7	719	9	US-09-764-848-12	Sequence 12, Appl
9	357.4	37.7	719	14	US-10-116-016-12	Sequence 24, Appl
10	357.4	37.7	719	14	US-10-103-313-247	Sequence 12, Appl
11	357.4	37.7	719	16	US-10-222-020-12	Sequence 570, Appl
12	317.8	33.6	400	21	US-10-505-680-570	Sequence 21320, A
13	232.4	24.5	253	9	US-09-864-761-21320	Sequence 10941, A
14	230.4	24.3	326	17	US-10-242-535A-10941	Sequence 10941, A
15	230.4	24.3	326	18	US-10-085-783A-10941	Sequence 571, Appl
16	197.8	20.9	467	21	US-10-505-680-571	Sequence 10204, A
17	167.4	17.7	470	9	US-09-864-761-10204	Sequence 54267, A
18	109.2	11.5	430	20	US-10-357-930-54267	Sequence 22728, A
19	97.6	10.3	466	10	US-09-918-995-22728	Sequence 4587, Ap
20	95.2	10.1	799	21	US-10-956-157-4587	Sequence 582, Appl
21	95.2	10.1	1033	9	US-09-954-531-582	Sequence 1649, Ap
22	95.2	10.1	1033	21	US-10-843-641A-1649	Sequence 35185, A
23	93.2	9.8	454	10	US-09-918-995-35185	Sequence 9822, Ap
24	89.6	9.5	600	21	US-10-956-157-9822	Sequence 20856, A
25	86.4	9.1	475	10	US-09-918-995-20856	Sequence 26844, A
26	75	7.9	75	9	US-09-864-761-26844	Sequence 12263, A
27	68.8	7.3	551	16	US-10-029-386-12263	Sequence 25964, A
28	61.2	6.5	186	16	US-10-029-386-25964	Sequence 29954, A
29	60.2	6.4	65	10	US-09-908-975-29954	Sequence 26081, A
30	57.8	6.1	969	20	US-10-363-345A-26081	Sequence 26082, A
31	57.8	6.1	969	21	US-10-363-345A-26082	Sequence 26081, A
32	57.8	6.1	969	21	US-10-363-483A-26081	Sequence 26082, A
33	57.8	6.1	2098	18	US-10-296-987-1	Sequence 1, Appl
34	52	5.5	535	20	US-10-363-345A-28883	Sequence 28883, A
35	51.6	5.4	535	20	US-10-363-345A-28884	Sequence 28884, A
36	51.6	5.4	535	21	US-10-363-483A-28884	Sequence 28883, A
37	51.6	5.4	535	21	US-10-363-483A-28884	Sequence 28884, A
38	51.4	5.4	788	20	US-10-363-345A-9298	Sequence 9297, Ap
39	51.4	5.4	788	20	US-10-363-345A-9298	Sequence 9298, Ap
40	51.4	5.4	788	21	US-10-363-483A-9298	Sequence 9297, Ap
41	51.4	5.4	788	21	US-10-363-483A-9298	Sequence 9298, Ap
42	51.4	5.4	788	21	US-10-363-483A-9298	Sequence 80472, A
43	48.6	5.1	350	20	US-10-425-115-80472	Sequence 120013, A
44	48.6	5.1	1062	20	US-10-425-115-120013	Sequence 182979, A
45	48	5.1	574	20	US-10-425-115-182979	

ALIGNMENTS

RESULT 1
US-10-489-740-35
; Sequence 35, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: p9
; FILE REFERENCE: Angiogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-35

Query Match 91.9%; Score 870; DB 21; Length 1128;
Best Local Similarity 98.0%; Pred. No. 2.8e-241;
Matches 879; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

Qy	24	GGAAATTCGGATCTCGAGGCCACGAGCCGCAACAGTCTGAAGCCCTTTAAATGCAGCA	83
Db	219	GGTTTTGGATTGTAGCGTCTGCACCTTCAGAAACAGTCTGAAGCCCTTTAAATGCAGCA	278
Qy	84	TCGCGATGTGAGGAGGACCTCCACACGAGAAACCTCGATCAATTTCTCAGCTGTGG	143
Db	279	TCTGCGATGTGAGGAGGACCTCCACACGAGAAACCTCGATCAATTTCTCAGCTGTGG	338

Qy	144	CNCAACAAAGTGGCAACAACAGTATGCCACACCCCTTAAAAACGAGAGAGAGAGA	203
Db	339	CGCAACAAAGTGGCAACAACAGTATGCCACCCCAACCCCTTAAAAAGGAGAGAGAGA	398
Qy	204	AAGTTTGAAAAGCAGGACAAGAGAGAAACCTGAGAAGAGCAAGGAATTTAGTCTTAGTGTTA	263
Db	399	AAGTTGAAAAGCAGGACAAGAGAGAAACCTGAGAAGAGCAAGGAATTTAGTCTTAGTGTTA	458
Qy	264	CCAAAGAAAAATACCAACAAGAAAAACCAAAACCAAAAGTCTGACATTTCTGAAAAGATCCTCCTTA	323
Db	459	CCAAAGAAAAATACCAACAAGAAAAACCAAAACCAAAAGTCTGACATTTCTGAAAAGATCCTCCTTA	518
Qy	324	GTGAAGCMAACAGCATACAGTCTGCAATGCTACAAACAAAGACAGCGAAACAAATCACA	383
Db	519	GTGAAGCMAACAGCATACAGTCTGCAATGCTACAAACAAAGACAGCGAAACAAATCACA	578
Qy	384	CCTCAAGGCCCGGCTGAAAAACGTGACAGGAGCACTGCACAGCAGCTTGGCAGTAACTG	443
Db	579	CCTCAAGGCCCGGCTGAAAAACGTGACAGGAGCACTGCACAGCAGCTTGGCAGTAACTG	638
Qy	444	TGGSCAACCGTCACCGTCAATTATCAACAGATTTTAAAGGAAAAAGACTCGCTCTCATCGACAT	503
Db	639	TGGSCAACCGTCACCGTCAATTATCAACAGATTTTAAAGGAAAAAGACTCGCTCTCATCGACAT	698
Qy	504	CCTCATCAACAGTACCTCCAGTCAGCGGTGAGAACAGCAGAACCCAGCAGCAGCTCGGGT	563
Db	699	CCTCATCAACAGTACCTCCAGTCAGCGGTGAGAACAGCAGAACCCAGCAGCAGCTCGGGT	758
Qy	564	CAGAGACACAGACAAGGGTCTCCCGTTCTTCACGCCAAAGGGGGAGACATGTCAGCAG	623
Db	759	CAGAGACACAGACAAGGGTCTCCCGTTCTTCACGCCAAAGGGGGAGACATGTCAGCAG	818
Qy	624	TCAAATGATGAATCTTTCTGAAAATTGACATGGAATTGTGAAAACTATGAATCAGGGTATG	683
Db	819	TCAAATGATGAATCTTTCTGAAAATTGACATGGAATTGTGAAAACTATGAATCAGGGTATG	878
Qy	684	AAATTCAAAACCTCCACCTGCCCATGTCTGTGGATCCCTGGAGAAATCTTCTGTGGACAT	743
Db	879	AAATTCAAAACCTCCACCTGCCCATGTCTGTGGATCCCTGGAGAAATCTTCTGTGGACAT	938
Qy	744	CGACCTCTTAGTGATGTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCACAG	803
Db	939	CGACCTCTTAGTGATGTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCACAG	998
Qy	804	GAAATTCGCAACCTGACGATTTACTCTTTGACACTTTTATGTATTCATTTGTTTATATGAT	863
Db	999	GAAATTCGCAACCTGACGATTTACTCTTTGACACTTTTATGTATTCATTTGTTTATATGAT	1058
Qy	864	TTTCCTTAACAATCAATTTATTAATTTGGATGTGCTCCGAAATCTACTTTTATTAATAAAA	920
Db	1059	TTTCCTTAACAATCAATTTATTAATTTGGATGTGCTCCGAAATCTACTTTTATTAATAAAA	1115

RESULT 2

US-10-505-680-569
; Sequence 569, Application US/10505680
; Publication No. US2005009592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.

FILE REFERENCE: 4239-64452
CURRENT APPLICATION NUMBER: US/10/505,680

; CURRENT APPLICATION NUMBER: US/10/505,680

; CURRENT FILING DATE: 2004-08-12

; PRIOR APPLICATION NUMBER: 60/357,031
 ; PRIOR FILING DATE: 2002-02-13

; PRIOR FILING DATE: 2002-02-13
 : NUMBER OF SEQ ID NOS: 822

; NUMBER OF SEQ ID NOS: 822
; SOFTWARE: PatentIn version

; SEQ ID NO 569

; LENGTH: 1036

1

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-680-569
```

Query Match 91.7%; Score 868.4; DB 21; Length 1036;

Best Local Similarity 97.9%; Pred. No. 7.8e-241;

Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Qy	24	GBAATTCGGATCTCCGAGGCCACGAAGCGCAACAGTGTCTGAAGCCTTTAAATGCAGCA	83
Db	135	GGTTTTGGGATTGTAGCGTCTGCACCTTGAAAACAGTGTCTGAAGCCTTTAAATGCAGCA	194
Qy	84	TCTCGCATGTGAGGAAAGCACCTCCAACAGAAAACTCGGATCAATTTCTAGCTGGTGG	143
Db	195	TCTCGCATGTGAGGAAAGCACCTCCAACAGAAAACTCGGATCAATTTCTAGCTGGTGG	254
Qy	144	CNCAAAGAATGGGCACAACAGTATGCCACCACCCACACCCCTTAATAAAGGAGAGAAAGGAGA	203
Db	255	CACAACAAGTGGGCACAACAGTATGCCACCACCCACACCCCTTAATAAAGGAGAGAAAGGAGA	314
Qy	204	AAGTTGAAAAGCAGGACAAAGAGAGAAACTTGAGAAAAAGACAAGGAAATTAGTCTTAGTGTTA	263
Db	315	AAGTTGAAAAGCAGGACAAAGAGAGAACTTGAGAAAAAGACAAGGAAATTAGTCTTAGTGTTA	374
Qy	264	CCAGAAAAATAACAACAAGAAAAACAACCAAAAGTCTGACATTTCTGAAAAGATCTCTCCTTA	323
Db	375	CCAGAAAAATAACAACAAGAAAAACAACCAAAAGTCTGACATTTCTGAAAAGATCTCTCCTTA	434
Qy	324	GTGAGCAACACAGCATACAGTCTGCAAAATGCTACAACAAGACACGAGAAACAAATCACA	383
Db	435	GTGAGCAACACAGCATACAGTCTGCAAAATGCTACAACAAGACACGAGAAACAAATCACA	494
Qy	384	CCTCAAGGCCCCCGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTTGGCAGTAAC TG	443
Db	495	CCTCAAGGCCCCCGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTTGGCAGTAAC TG	554
Qy	444	TGGGCAACGTCACCGTCATTATCACAGACTTTAAGAAAAGACTCGCTCCTCATCCACAT	503
Db	555	TGGGCAACGTCACCGTCATTATCACAGACTTTAAGAAAAGACTCGCTCCTCATCCACAT	614
Qy	504	CCTCATCCACAGTGA C C T C C A G T C G A G G G T C A G A A C A G A A C C A G A S C A G T C G G G G T	563
Db	615	CCTCATCCACAGTGA C C T C C A G T G C A G G G T C A G A A C A G A R A C C A G A G C A G T C G G G G T	674
Qy	564	CAGAGAGCACAACAAGGGTCTCTCCGGTCTTCBACGCGCAAGGGCGCACATGTCAGCAG	623
Db	675	CAGAGAGCACAACAAGGGTCTCTCCGGTCTTCBACGCGCAAGGGCGCACATGTCAGCAG	734
Qy	624	TCBAATGATGAATCTTTCTGAAATTTGCACATGGAAATTTGTGAAAACACTATGAATCAGGGTATG	683
Db	735	TCBAATGATGAATCTTTCTGAAATTTGCACATGGAAATTTGTGAAAACACTATGAATCAGGGTATG	794
Qy	684	AAATTTCAAAACCTCCACCTGCCATGCTGTGCATCCCTGGAGAACTTTCTGTGGACAT	743
Db	795	AAATTTCAAAACCTCCACCTGCCATGCTGTGCATCCCTGGAGAACTTTCTGTGGACAT	854
Qy	744	CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGGCCAACAG	803
Db	855	CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGGCCAACAG	914
Qy	804	GAAATTTGCGACCTCGACGATTACTCTTGACACTTTTATGTATTTCCATTTGTTTATATGAT	863
Db	915	GAAATTTGCGACCTCGACGATTACTCTTGACACTTTTATGTATTTCCATTTGTTTATATGAT	974
Qy	864	TTTCCTTAACAATCATTTATAATTTGGAATGTGCTCCTGAAATCTACTTTTATAAAAAA	920
Db	975	TTTCCTTAACAATCATTTATAATTTGGAATGTGCTCCTGAAATCTACTTTTATAAAAAA	1031

RESULT 3

US-10-956-157-1792

; Sequence 1792, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956.157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1792
 ; LENGTH: 1036
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-956-157-1792

Query Match 91.7%; Score 868.4; DB 21; Length 1036;
 Best Local Similarity 97.9%; Pred. No. 7.8e-241;
 Matches 878; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

QY	24	GGAATTCGGATCTCTCGAGGCCACGAAAGGCCGAGAACAGTGTCTGAAGCCCTTTAAATGCAGCA	83
DB	135	GGTTTTGGGATTTGAGCTCTGACCTTTCAGAAACAGTGTCTGAAGCCCTTTAAATGCAGCA	194
QY	84	TCTGCGATGTGAGGAAGGCGACCTCCACGAGAAACCTTCGGATCAATTTCTCAGCTGGTGG	143
DB	195	TCTGCGATGTGAGGAAGGCGACCTCCACGAGAAACCTTCGGATCAATTTCTCAGCTGGTGG	254
QY	144	CNCAACAAGTGCCACACAGATATGTCACCCACACACCCCTTAAAGGAGGAGGAGGAGA	203
DB	255	CACAACAAGTGCCACACAGATATGTCACCCACACCCCTTAAAGGAGGAGGAGGAGA	314
QY	204	AAGTTGAAAGCAGGACCAAGAAACCTTGAGAAAGACAAGGAAATTAGTCTTAGTGTTA	263
DB	315	AAGTTGAAAGCAGGACCAAGAAACCTTGAGAAAGACAAGGAAATTAGTCTTAGTGTTA	374
QY	264	CCAAGAAATATACCAACGAGAAACCAACCAAGTCTGACATTTCTGAAGATCTCTCTCA	323
DB	375	CCAAGAAATATACCAACGAGAAACCAACCAAGTCTGACATTTCTGAAGATCTCTCTCA	434
QY	324	GTGAGCAACACGACATACAGTCTGCAATGCTTACAAACAAAGACGACGAAACCAATCACA	383
DB	435	GTGAGCAACACGACATACAGTCTGCAATGCTTACAAACAAAGACGACGAAACCAATCACA	494
QY	384	CCTCAAGGCCCGGCTGAAAAACGTTGGAAGGAGCACTGCACAGACGATTTGGCAGTAACTG	443
DB	495	CCTCAAGGCCCGGCTGAAAAACGTTGGAAGGAGCACTGCACAGACGATTTGGCAGTAACTG	554
QY	444	TGGGCAACGTACCGTCAATATACAGATTTAAGAAAAAGACTCGCTCTCTCATCGACAT	503
DB	555	TGGGCAACGTACCGTCAATATACAGATTTAAGAAAAAGACTCGCTCTCTCATCGACAT	614
QY	504	CCTCATCCACGTGACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGACGCTCGGGGT	563
DB	615	CCTCATCCACGTGACCTCCAGTGCAGGCTCAGAACAGCAGAACCCAGACGCTCGGGGT	674
QY	564	CAGAGAGCACAGAACGGGCTCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCCAGCAG	623
DB	675	CAGAGAGCACAGAACGGGCTCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCCAGCAG	734
QY	624	TCAATGATGAATCTTTCTGAAATTCACATGGAATTTGTGAAAACTATGATCAGGGTATG	683
DB	735	TCAATGATGAATCTTTCTGAAATTTGACATGGAATTTGTGAAAACTATGATCAGGGTATG	794
QY	684	AAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGGAGATCTTCTGTGGACAT	743
DB	795	AAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCCTGGGAGATCTTCTGTGGACAT	854
QY	744	CGACCTCTTAGTGATGCTGCGAGATAATTTCTGTGTTTGGCCATGCTGGCCACCAAG	803
DB	855	CGACCTCTTAGTGATGCTGCGAGATAATTTCTGTGTTTGGCCATGCTGGCCACCAAG	914
QY	804	GAAATTCGCAACCCCTGACGATTAATCTTGACACTTTTATGATATTCATGTTATATGAT	863

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Db      915   GAATTTGCGACCCGTGAGATTACTCTTGACACTTTTAATGTAATTCCTGGTATATATGAT 974
Qy      864   TTTTCTAACCAATCATTTATAATTGGAATGCTCCTGGAATCTACTTTTATAAAAAA 920
Db      975   TTTTCTAACCAATCATTTATAATTGGAATGCTCCTGGAATCTACTTTTATAAAAAA 1031

RESULT 4
US-10-956-157-7027
; Sequence 7027, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7027
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7027
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Query Match	91.7%;	Score 868.4;	DB 21;	Length 1036;
Best Local Similarity	97.9%;	Prod. No. 7.8e-241;	Indels 0;	Gaps 0;
Matches 878;	Conservative 1;	Mismatches 18;		
QY	24	GGAAATTCGGATCTCTCGAGGCCACGAAGGCCGCAAAACAGTGTCTGAAGCCCTTTAAATCGACGA	83	
Db	135	GGTTTTGGATTTAGCGTCTGCACCTTCAGAAACAGTGTCTGAAGCCCTTTAAATCGACGA	194	
QY	84	TCTGCGATGTGAGAAAGGCACTTCCACAGAGAAACCTTCGGATCAATTTCTCAGCTGGTGG	143	
Db	195	TCTGCGATGTGAGAAAGGCACTTCCACAGAGAAACCTTCGGATCAATTTCTCAGCTGGTGG	254	
QY	144	CNCAACAAAGTGCACAACAGTATGCCACCCACACCCCTTAAAAAGGAGAAAGAGAGA	203	
Db	255	CACAAACAAGTGCACAACAGTATGCCACCCACACCCCTTAAAAAGGAGAAAGAGAGA	314	
QY	204	AAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTA	263	
Db	315	AAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAGACAAGGAAATTTAGTCTCTAGTGTTA	374	
QY	264	CCAGAAAATACCACCAACAGAGAAAACCAACCAAGTCTTGACATCTCTGAAAAGATCTCTCTTA	323	
Db	375	CCAGAAAATATCCAAACAGAGAAAACCAACCAAGTCTTGACATCTCTGAAAAGATCTCTCTTA	434	
QY	324	GTGAAGCAAAACAGCATACAGTCTGCAAAATGTCTACAACAAAGACGACGAGAAACAAATCACA	383	
Db	435	GTGAAGCAAAACAGCATACAGTCTGCAAAATGTCTACAACAAAGACGACGAGAAACAAATCACA	494	
QY	384	CCTCAAGGCCCGGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTAACTG	443	
Db	495	CCTCAAGGCCCGGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTAACTG	554	
QY	444	TGGGCAACGTCACCGCTATTATCACAGACTTTTAAAGGAAAAGACTCGCTCTCTCATCGACAT	503	
Db	555	TGGGCAACGTCACCGCTATTATCACAGACTTTTAAAGGAAAAGACTCGCTCTCTCATCGACAT	614	
QY	504	CCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGAAACCCAGACAGCTCGGGGT	563	
Db	615	CCTCATCCACAGTGACCTCCAGTGCAGGGTTCAGAACAGCAGAAACCCAGACAGCTCGGGGT	674	
QY	564	CAGAGGACACAGCAAGGGCTCCTCCGTTCTCTCACGCGCAAGGGCGACATGTTCAGCAG	623	
Db	675	CAGAGGACACAGCAAGGGCTCCTCCGTTCTCTCACGCGCAAGGGCGACATGTTCAGCAG	734	
QY	624	TCAATGATGAATCTTTCTGAAAATTGCAATGCAATGGAATTTGTGAAAACCTATGAATCAGGGTATG	683	

Db 735 TCAATGATGATCTTTCTGAAATTCACATGGAATTTGTGAAACTATGATCAGGGTATG 794
Qy 684 AAATTTAAAACCTCCACCTGCCCATGCTGTGATCCCTCGAGAAATCTTCTGTGACAT 743
Db 795 AAATTTAAAACCTCCACCTGCCCATGCTGTGATCCCTCGAGAAATCTTCTGTGACAT 854
Qy 744 CGACCTCTTAGTATGATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 803
Db 855 CGACCTCTTAGTATGATGCTGCCAGGATAATTTCTGCTTGGCATGGGCATCTGGCCACCAAG 914
Qy 804 GAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATTTATGATTTATGAT 863
Db 915 GAATTTGCGACCTCGACGATTAATCTTGACACTTTTATGATTTATGATTTATGAT 974
Qy 864 TTTCTTAACAATCATTTATTAATTTGGATGCTCTCTGAATCTACTTTTTATAAAAAA 920
Db 975 TTTCTTAACAATCATTTATTAATTTGGATGCTCTCTGAATCTACTTTTTATAAAAAA 1031

RESULT 5

US-10-103-313-121
; Sequence 121, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FUZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-121

Query Match 90.7%; Score 859; DB 14; Length 2156;
Best Local Similarity 97.9%; Pred. No. 6.4e-238;
Matches 879; Conservative 1; Mismatches 17; Indels 1; Gaps 1;
Qy 24 GGAATTCGGATCTCGAGGCCACGAGGCCGGAACAGTCTGAAGCCTTTAAATGACGA 83
Db 64 GGTTTGGGATTTAGCGCTGTCACCTTCAGAAACAGTCTGAAGCCTTTAAATGACGA 123
Qy 84 TCTGCGATGTGAGAAAGGCACCTCCACCA-GAAACCTCGGATCAATCTCAGCTGGTG 142
Db 124 TCTGCGATGTGAGAAAGGCACCTCCACCATGAAACCTCGGATCAATCTCAGCTGGTG 193
Qy 143 GCNCAACAGTGGCACAACAGTATGCCACCCACCCCTAAAAAGGAGAAAGAGGAG 202
Db 184 GCACAACAGTGGCACAACAGTATGCCACCCACCCCTAAAAAGGAGAAAGAGGAG 243
Qy 203 AAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATTAGTCTAGTGT 252
Db 244 AAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATTAGTCTAGTGT 303
Qy 263 ACCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCT 322
Db 304 ACCAAGAAAATACCAACAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCT 353
Qy 323 AGTGAAGCAACAGCATACAGTCTGCAATTTGCTACAAAGACCAAGGCAAAACAAATCAC 382
Db 364 AGTGAAGCAACAGCATACAGTCTGCAATTTGCTACAAAGACCAAGGCAAAACAAATCAC 423
Qy 383 ACCTCAAGGCCCGGTGAAAAAGCTGGACAGGACCTGCCACAGATTTGGCAGTAAT 442
Db 424 ACCTCAAGGCCCGGTGAAAAAGCTGGACAGGACCTGCCACAGATTTGGCAGTAAT 483
Qy 443 GTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAGACTCGCTCTCATCGACA 502

Db 484 GTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAGAGACTCGCTCTCATCGACA 543
Qy 503 TCTCTATCACAGTGAACCTCCAGTCAGGGTCAGAAACACAGAACCCAGASCAGCTCGGG 562
Db 544 TCTCTATCACAGTGAACCTCCAGTCAGGGTCAGAAACACAGAACCCAGASCAGCTCGGG 603
Qy 563 TCAGAGAGACACAGAACGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTCAGCA 622
Db 604 TCAGAGAGACACAGAACGGGCTCTCCCGTCTCTCCACGCCAAAGGGCGACATGTCAGCA 663
Qy 623 GTCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAACCTATGAATCAGGGTAT 682
Db 664 GTCAATGATGAATCTTTCTGAAATTCACATGGAATTTGAAACCTATGAATCAGGGTAT 723
Qy 683 GAAATTTAAAACCTCCACCTGCCCATGCTGTGATTCCTGCGAGAAATCTTCTGTGACGA 742
Db 724 GAAATTTAAAACCTCCACCTGCCCATGCTGTGATTCCTGCGAGAAATCTTCTGTGACGA 783
Qy 743 TCGACCTCTTAGTATGATGCTGCCAGGATAATTTCTGCTTGCATGCGCATCTGGCCACCA 802
Db 784 TCGACCTCTTAGTATGATGCTGCCAGGATAATTTCTGCTTGCATGCGCATCTGGCCACCA 843
Qy 803 GGAATTTGCAACCTCCACCTGACGATTAATCTTGACACTTTTATGATTTGATTTATATGA 862
Db 844 GGAATTTGCAACCTCCACCTGACGATTAATCTTGACACTTTTATGATTTGATTTATATGA 903
Qy 863 TTTTCTTAACAATCATTTATTAATTTGGATGCTGCTGGAATCTACTTTTTATAAAAAA 920
Db 904 TTTTCTTAACAATCATTTATTAATTTGGATGCTGCTGGAATCTACTTTTTATAAAAAA 961

RESULT 6

US-09-918-995-24859
; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24859
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(502)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24859

Query Match 49.6%; Score 469.6; DB 10; Length 502;
Best Local Similarity 96.6%; Pred. No. 2.6e-125;
Matches 478; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 337 CATACAGTCTGCAATGCTTACAAAGACCAAGACCAAGGCAAAACAAATCACACCTCAAGGCCCG 396
Db 8 CNAATAGATCGCTATAGCGCTTCGAGGACCAAGGCAAAACAAATCACACCTCAAGGCCCG 67
Qy 397 GCTGAAAAACGTGGACAGGACCTGCCACAGCAGTTGGCAGTAATCTGTGGCAACGTCAC 456
Db 68 GCTGAAAAACGTGGACAGGACCTGCCACAGCAGTTGGCAGTAATCTGTGGCAACGTCAC 127
Qy 457 CGTCAATATCACAGCTTTTAAGAAAAAGACTCGCTCTCATCGACATCTCATCCAGT 516
Db 128 CGTCAATATCACAGCTTTTAAGAAAAAGACTCGCTCTCATCGACATCTCATCCAGT 187
Qy 517 GACCTCCAGTCAGGGTCAGAAACAGCAGAACCAAGCAGCTCGGGGTGAGAGACAGACA 576

188 GACCTCAGTGCAGGGTTCAGAAACAGCAGCAAGACGAGCAGCTCGGGGTTCAGAGAGCAGCA 247
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637 TTCTGAAATTCACATGGAATTCGAAACTATGAATCAGGGTATGAAATTCAAAACCT 696
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757 ATGCTGCAGATGAATTCCTGCTGTCATCCCTGGAAGATTCCTCTGTGACATCGACCTCTTAGTG 816
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817 TGACGATTACTCTTG 831
488 TGACGATTACTCTTG 502

RESULT 7
US-09-864-761-4575/c
; Sequence 4575, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4575
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012553.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
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Best Local Similarity 99.8%; Pred. No. 1.9e-113;
Matches 428; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 461 ATTATCAGACACTTTAAGGAAAGACTCGCTCTCATCGACATCTTCATCCACAGTGACC 520
DB 369 ATTATCAGACACTTTAAGGAAAGACTCGCTCTCATCGACATCTTCATCCACAGTGACC 310
QY 521 TCCAGTGCAGGGTCAGAAACAGCAGCAAGCAGCAGCTCGGGGTTCAGAGAGCAGCAAG 580
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QY 581 GGCTCTCTCCGTTCTTCCAGCGCCAAAGGGCGACATGTCAGCAGTCAATGATGATCTTTC 640
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DB 129 CTGCCATGCTGCTGTCATCCCTGGAGAACTTCTGTGGACATCGACCTCTTAGTGATGC 70
QY 761 TGCAGGATAATTTCTGCTTGCATGGGCAATCTGTGGCCACCAAGAAATTCGACCCCTGAC 820
DB 69 TGCAGGATAATTTCTGCTTGCATGGGCAATCTGTGGCCACCAAGAAATTCGACCCCTGAC 10
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DB 9 GATTACTCT 1
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US-09-764-848-12
; Sequence 12, Application US/09764848
; Patent No. US2002007270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ08
; CURRENT APPLICATION NUMBER: US/09/764,848
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 719

; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-08-22
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
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; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08

Query Match 37.7%; Score 357.4; DB 16; Length 719;
Best Local Similarity 94.4%; Pred. No. 1.2e-92;
Matches 389; Conservative 2; Mismatches 19; Indels 2; Gaps 2;

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DB	53	GGTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGACGA	112
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DB	113	TCGCGATGTGAGGAAAGGACCTCCACCAGAAAACTCGGATCAATTTCTCAGCTGGTG	172
QY	144	CNCAACAGTGGCACAAACAGTATGCCCCACCACCCCTTAAAAAGGAGAGAGAGA	203
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QY	204	AGTTCAAGGAGGACAAAGACCTGAGAAACCAAGCAAGCAAGCAAGCAAGCAAGCA	263
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QY	264	CCAAGAAAAATACCAACAGAAAAACCAAAAGTCTGACATTTCTGAAAGATCCTCCTA	323
DB	293	CCAAGAAAAATACCAACAGAAAAACCAAAAGTCTGACATTTCTGAAAGATCCTCCTA	351
QY	324	GTGAAGCAACAGCATACTAGTCTGAAATGCTACAAACAGACCGGAGAAACAAATCACA	383
DB	352	GTGAAGCAACAGCATACTAGTCTGAAATGCTACAAACAGACCGGAGAAACAAATCACA	411
QY	384	CCTCAAGGCGCGGCTGAAACAGT-GGACAGGACACTGCACAGCAGTTGG	434
DB	412	CCTCAAGGCGCGGCTGAAACAGTGGGACAGGACACTGCACAGCAGTTGG	463

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US-10-505-680-570/C
; Sequence 570, Application US/10505680
; Publication No. US2005009592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the
; Secretary of the Department of Health and Human Services
; APPLICANT: Jazaeri, Amir A.
; APPLICANT: Boyd, Jeff
; APPLICANT: Liu, Edison T.
; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
; FILE REFERENCE: 4239-64452
; CURRENT APPLICATION NUMBER: US/10/505,680


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; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is a, c, g, or t
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; US-10-242-535A-10941

Query Match          24.3%; Score 230.4; DB 17; Length 326;
Best Local Similarity 93.4%; Pred. No. 5.1e-56;
Matches 240; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 250 AAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGCAAGGAAATTTAGTCTAGTGTTA 309

Qy 264 CCAAGAAAAATACCAAC 280
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; Sequence 10941, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13

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; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10941
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
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; US-10-085-783A-10941

Query Match          24.3%; Score 230.4; DB 18; Length 326;
Best Local Similarity 93.4%; Pred. No. 5.1e-56;
Matches 240; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 24 GGAATTCGGATCTCGAGGCCACGAAGCCGAAACAGTGTGCTGAAGCCTTTAAATGCAGCA 83
Db 70 GGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGTGCTGAAGCCTTTAAATGCAGCA 129

Qy 84 TCTCGATGTGAGAAAGGACCTCCACGAGAAACCTCGGATCAATTCTCAGCTGGTG 143
Db 130 TCTCGATGTGAGAAAGGACCTCCACGAGAAACCTCGGATCAATTCTCAGCTGGTG 189

Qy 144 CNCAACAAGTGGCACACAGTATGCCACCCACCCACCCCTTAAAGGAGGAAGAGGA 203
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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
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- 7: gb_ph.*
- 8: gb_pl.*
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- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1129.4	99.9	1131	6	AX138332 Sequence
5	1021	90.3	3641	6	BD209971 Human tra
6	1019.4	90.1	1036	6	AX821956 Sequence
7	1019.4	90.1	1036	6	AF179286 Homo sapi
8	1019.4	90.1	1128	9	BC014959 Homo sapi
9	1019.4	90.1	2344	9	BC036459 Homo sapi
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12	934.4	82.6	936	9	AF227959 Homo sapi
13	930.4	82.3	943	6	C0715417 Sequence
14	881.4	77.9	947	6	AX092138 Sequence
15	881.4	77.9	947	6	AX114151 Sequence
16	881.4	77.9	947	6	AX138318 Sequence
17	881.4	77.9	947	6	AX138324 Sequence
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ALIGNMENTS

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DEFINITION Sequence 5 from Patent EP1108785.
ACCESSION AX114152
VERSION AX114152.1 GI:140311160

KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Apoptin-associating protein
TITLE Patent: EP 1108785-A 5 20-JUN-2001;
JOURNAL Leadd B.V. (NL)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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Db	1	TATAACTATCTATTTCGATGATGAAGATACCCACCAAAACCAAAAGAGATCTGGAAT	60			
Qy	61	TCGGATCCTCGAGCCACGAAGCGCTTCTCCTCGAGCGCGCGCTTTCGGCTTGGG	120			
Db	61	TCGGATCCTCGAGCCACGAAGCGCTTCTCCTCGAGCGCGCGCTTTCGGCTTGGG	120			
Qy	121	GGGCGGGGTACAGCCATCCATGACCATGGGCGACAAAGAGCCCGACAGCCCAAAA	180			
Db	121	GGGCGGGGTACAGCCATCCATGACCATGGGCGACAAAGAGCCCGACAGCCCAAAA	180			
Qy	181	AGACAAGCGAAACCTCGCGCAGACGAAGGGTTTGGGATTTGTAGCGTCTGCACCTTCA	240			

PAT 11-MAY-2001

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LOCUS AX092139 1131 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 9 from Patent WO0116165.
ACCESSION AX092139
VERSION AX092139.1 GI:13444366
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Noteborn, M.H. and danen-van Oorschot, A.A.
Apoptin-associating protein
Patent: WO 0116165-A 9 08-MAR-2001;
Leadd B.V. (NL)
FEATURES
source 1. .1131
Location/Qualifiers
misc_feature 1. .1131
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RESULT 3
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LOCUS
DEFINITION
Sequence 9 from Patent EP1083224.
ACCESSION
AX138319
VERSION
AX138319.1
KEYWORDS
GI:14274285
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Noteborn, M.H. and danen-van Oorschot, A.A.
Apoptin-associating protein
Patent: EP 1083224-A 9 14-MAR-2001;
Leadd B.V. (NL)
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misc_feature
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Best Local Similarity 99.9%; Pred. No. 1.4e-290;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4
AX138332
LOCUS
DEFINITION
Sequence 12 from Patent EP1081226.
ACCESSION
AX138332
VERSION
AX138332.1
KEYWORDS
GI:14274288
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. Apoptin-associating protein
Patent: EP 1081226-A 12 07-MAR-2001;
Leadd B.V. (NL)

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LOCUS		Human transcriptional regulator molecules.	
DEFINITION		BD209971	
ACCESSION		BD209971.1 GI:33019741	
VERSION		JP 2002513554-A/43.	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
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REFERENCE		1 (bases 1 to 3641)	
AUTHORS		Hillman,J.L., Bandman,O., Lal,P., Yue,H., Reddy,R., Tang,T.Y., Gerstein,E.H., Patterson,C., Baughn,M.R., Azimzal,Y. and Lu,D.A.M.	
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JOURNAL		Patent: JP 2002513554-A 43 14-MAY-2002; INCYTE PHARMACEUTICALS INC	
COMMENT		OS Homo sapiens (human) PN JP 2002513554-A/43 PD 14-MAY-2002 PF 04-MAY-1999 JP 2000547113 PR 05-MAY-1998 US 60/084254,07-AUG-1998 US 60/095827 PR 02-OCT-1998 US 60/102745 PI JENNIFER L HILLMAN,OLGA BANDMAN,PREETI LAL,HENRY YUE,ROOPA PI REDDY. PI TOM Y TANG,EDWARD H GERSTEIN,CHANDRA PATTERSON,MARIAH R BAUGHN, PI YALDA AZIMZAL,DYUNG AINA M LU PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/02,A61P43/00, PC C07K14/47, PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68//C12P21/ PC 02, PC C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC Incyte clone 3149729CB1 FH Key Location/Qualifiers FT source 1. .3641 FT /organism='Homo sapiens (human)'. FT Location/Qualifiers 1. .3641 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
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RESULT 6
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LOCUS
DEFINITION
ACCESSION
VERSION
AX821956
Sequence 84 from Patent W003068961.
AX821956
AX821956.1 GI:39725177
linear PAT 10-DEC-2003

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Query Match 90.1%; Score 1019.4; DB 6; Length 1036;
Best Local Similarity 99.4%; Pred. No. 3.5e-261;
Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DEFINITION
AF179286
VERSION AF179286.1 GI:5802963
KEYWORDS
SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1036)
Zheng,L.X., Schickling,O., Peter,M.E. and Lenardo,M.J.
The death effector domain-associated factor plays distinct
regulatory roles in the nucleus and cytoplasm
J. Biol. Chem. 276 (34), 31945-31952 (2001)
21402885
PUBMED 11395500
REFERENCE 2 (bases 1 to 1036)
Zheng,L.X., Yoo,T. and Lenardo,M.J.
A novel protein associated with Caspase-10 DED domain
Unpublished
3 (bases 1 to 1036)
Zheng,L.X., Yoo,T. and Lenardo,M.J.
Direct Submission
Submitted (20-AUG-1999) NIAID/NIH, 9000 Rockville Pike,
Bethesda, MD 20892, USA
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KEYWORDS	BC014959.1 GI:15928992
SOURCE	MGC.
ORGANISM	Homosapiens (human)
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AUTHORS	1 (bases 1 to 1128)
	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
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	Schneerch A., Schein J.E., Jones S.J. and Marra M.A.
	Generation and initial analysis of more than 15,000 full-length
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TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL	12477932
PUBMED	2 (bases 1 to 1128)
REFERENCE	Strausberg R.
AUTHORS	Direct Submission
TITLE	Submitted (01-OCT-2001) National Institutes of Health, Mammalian
JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
	USA.
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk
	Email: cgapbs@mail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Genome Sequence Centre,
	BC Cancer Agency, Vancouver, BC, Canada
	info@bcgsc.bc.ca
	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
	Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
	Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
	Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
	Teika Olson, Diana Palquist, Anca Petrescu, Anna Liisa Prabhu,
	Farvanah Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
	Duane Smalish, Jeff Stott, Miranda Teal, George Yang, Jacqui
	Schein, Asim Siddiqui, Rob Holt, Marco Marra.
	Clone distribution: MGC clone distribution information can be found
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VERSION
AY228125.1 GI:29423710
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Voekamp,P., Seelen,M.C., van Milteneburg,M.H., Bolk,M.W., Tait,S.W., Boesen-de Cock,J.G., Rohn,J.L., Borst,J. and Noteborn,M.H.
Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell killing
Cell Death Differ. 11 (5), 564-573 (2004)
14765135
2 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Boesen-de Cock,J.G.R., Borst,J. and Noteborn,M.H.M.
AAP-1, a binding partner of Apoptin, induces cell death in human tumor cells but not in normal diploid cells
Unpublished
3 (bases 1 to 1021)
Danen-van Oorschot,A.A.M., Boesen-de Cock,J.G.R., Borst,J. and Noteborn,M.H.M.
Direct Submission
Submitted (31-JAN-2003) Leadd BV, Wassenaarseweg 72, Leiden 2333 AL, The Netherlands
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RESULT 14
AX092138
LOCUS AX092138
DEFINITION Sequence 8 from Patent WO0116165.
ACCESSION AX092138
VERSION AX092138.1 GI:13444365
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Noteborn, M.H. and danen-van Oorschot, A.A.
TITLE Apoptin-associating protein
JOURNAL Patent: WO 0116165-A 8 08-MAR-2001;
Leadd B.V. (NL)
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/db_xref="taxon:9606"
misc_feature 1..947
/note="AAP-1-a nucleic acid wherein N can be A, C, G or T."
ORIGIN
Query Match 77.9%; Score 881.4; DB 6; Length 947;
Best Local Similarity 97.6%; Pred. No. 2.8e-224;
Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;
Qy 209 GGTTTTGGGATTTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCAGCA 268
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Qy 329 CACAACAGTGGCACAACAGATATGCCACCCACCCACCCCTTAAAAAGGAGAAAGAGAGA 388
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Qy 389 AGTTGAAAGCAGGACAAAGAAACCTGAGAAAGCAAGGAAATTTAGTCTAGTGTGA 448
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Qy 629 TGGGCAACGTACCGCTCATTTATCAGACATTTTAAAGGAAAGACTCGCTCTCATCGACAT 688
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RESULT 15
AX114151
LOCUS AX114151 947 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 4 from Patent EP1108785.
ACCESSION AX114151
VERSION AX114151.1 GI:14031159
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Apoptin-associating protein
TITLE Patent: EP 1108785-A 4 20-JUN-2001;
JOURNAL Leadd B.V. (NL)
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misc_feature 1..947
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ORIGIN

Query Match 77.9%; Score 881.4; DB 6; Length 947;
Best Local Similarity 97.6%; Pred. No. 2.8e-224;
Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;

Qy 209 GGTTTTGGGATGTAGCGCTGTGACCTTCAGAAAACAGTGTGAAGCCCTTTAAATGCAGCA 268
Db 24 GGAATTTGGATCTCTGAGGCCACAGAGCCGAAACAGTGTGAAGCCCTTTAAATGCAGCA 83
Qy 269 TCTGCGATGTGAGGAAAGGCCACCTCCACCAAGAAAACCTCGGATCAATTTCTCAGCTGTGG 328
Db 84 TCTGCGATGTGAGGAAAGGCCACCTCCACCAAGAAAACCTCGGATCAATTTCTCAGCTGTGG 143
Qy 329 CACAACAGTGGGACACAGTATGCGACCCACCACCCCTTAAAAAGGAGNAGGAGGA 388
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Qy 389 AAGTTGAAAACGACGACAAAGAGAAAACCTGAGAAAGCAAGCAATAGTCTAGTGTTA 448
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Qy 569 CCTCAAGGCCCGGCTGAAAACGTGGACAGGACCTGACAGCAGTGGCAGTAACTG 628
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- 13: geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1129.4	99.9	1131	4	Aaf55596 Nucleotid
2	1129.4	99.9	1131	4	Aaf55405 Nucleotid
3	1129.4	99.9	1131	5	Aaf57185 Apoptin-a
4	1021	90.3	3641	3	Aa52452 HTRM Clon
5	1019.4	90.1	1036	10	Adk66994 Gene #84
6	1019.4	90.1	1036	10	Adk66994 Gene #84
7	1019.4	90.1	1036	10	Adk66994 Gene #84
8	1017.8	90.0	1128	8	Adf34480 Gene enco
9	935.8	82.7	2156	4	Adf34480 Gene enco
10	935.8	82.7	2156	10	Adc46035 Human neo
11	881.4	77.9	947	4	Aaf55595 Nucleotid
12	881.4	77.9	947	5	Aaf55404 Nucleotid
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14	522.4	46.2	1501	5	Aa587102 DNA enco
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17	436	38.5	719	4	Adk43152 CDNA enco
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C	21	427.4	37.8	429	4	AAI36109	Aai36109 Probe #47
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C	25	427.4	37.8	429	4	AAK04634	Aak04634 Human bra
C	26	427.4	37.8	429	4	ABS29793	Ab29793 Human liv
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C	32	332.8	20.6	253	4	AAI23937	Aai23937 Probe #13
C	33	332.8	20.6	253	4	ABA69056	Ab69056 Human foe
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C	35	332.8	20.6	253	4	ABA51067	Ab51067 Human bre
C	36	332.8	20.6	253	4	ABA36000	Ab36000 Probe #14
C	37	332.8	20.6	253	4	AAK43164	Aak43164 Human bon
C	38	332.8	20.6	253	4	AAK17369	Aak17369 Human bra
C	39	332.8	20.6	253	4	ABS42798	Ab42798 Human liv
C	40	332.8	20.6	253	5	AAI09536	Aai09536 Probe #95
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C	42	168.4	14.9	470	4	AAI13037	Aai13037 Probe #29
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ALIGNMENTS

RESULT 1

AAF55596
ID AAF55596 standard; cDNA; 1131 BP.

AC AAF55596;

DT 29-MAY-2001 (first entry)

DB Nucleotide sequence of apoptin-associating protein 1 cDNA clone b.

KW Apoptin-associating protein; AAP; apoptosis; cell proliferation;
cell death; autoimmune disease; cancer; ss.

OS Homo sapiens.

PN WO200116165-A2.

PD 08-MAR-2001.

PF 01-SEP-2000; 2000WO-NL000612.

PR 02-SEP-1999; 99EP-00202858.

PR 21-OCT-1999; 99EP-00203465.

XX (LEAD-) LEADD BV.

XX Noteborn MHM, Danen-Van Oorschot AAAM;

XX WPI; 2001-235090/24.

XX New nucleic acids encoding apoptin-associating proteins useful for
inducing apoptosis, particularly p53 independent apoptosis, or for
treating cancers or autoimmune diseases.

XX Claim 6; Fig 2; 50pp; English.

XX The present sequence encodes a human apoptin-associating protein 1
(AAP1). The protein is capable of providing apoptosis. AAP polypeptides
and polynucleotides are useful for inducing apoptosis, particularly when
apoptosis is p53-independent. They may be used to produce pharmaceutical
compositions which are used for treating a disease where enhanced cell
proliferation or decreased cell death is observed, particularly in cancer
or in autoimmune diseases, for diagnosing a disease related with

CC aberrancies in the apoptotic process, and for detecting the presence of
CC cancer cells or cells that are prone to cancer
XX
SQ Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
Query Match 99.9%; Score 1129.4; DB 4; Length 1131;
Best Local Similarity 99.9%; Pred. No. 3e-310;
Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAAAACCAAAAGAGATCTGGAAT 60
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Db 661 AAGGAAAAGACTCGCTCTCTATCGACATCTCTATCCACAGTGACCTCCAGTGCAGGGTCA 720
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Qy 841 AATTGTGAAAACATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTT 900
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Qy 961 TGCTTCCCATGGSCATCTGGCCACCAGGAATTTCCGACCCCTGACGATTACTCTTGACAC 1020
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RESULT 2
AAF55405 standard; DNA; 1131 BP.
XX AAF55405;
XX AC
XX DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of an apoptin-associating protein.
DE DE Apoptin-associating proteinaceous substance; cell proliferation;
XX Apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW Apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
KW autoimmune disease; 88.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1. .828
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FT FT CDS 829. .939
FT /tag= b
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XX EF1081226-A1.
PN 07-MAR-2001.
XX PD
XX PF 02-SEP-1999; 99EP-00202858.
XX PR 02-SEP-1999; 99EP-00202858.
XX (LEAD-) LEADD BV.
XX WPI; 2001-219813/23.
DR P-PSDB; AAB67559, AAB67560, AAB67561, AAB67562, AAB67563.
XX PT Novel isolated or recombinant apoptin-associating proteinaceous
PT substance, apoptin-associating protein 1, useful for inducing apoptosis
PT for treating cancer or autoimmune diseases caused by aberrant apoptosis.
XX PS Claim 4; Fig 2; 29pp; English.
XX CC The present sequence encodes an apoptin-associating proteinaceous
CC substance (apoptin-associating protein 1 (AAP-1)), which is capable of
CC inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for
CC inducing a p53-independent apoptosis. They are used for treating a
CC disease where enhanced proliferation or decreased cell death is observed
CC e.g. cancer or autoimmune disease. They are also used for diagnosis of
CC diseases related with aberrations in the apoptotic process such as cancer
CC and autoimmune diseases

XX	Sequence	1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
SQ	Query Match	99.9%; Score 1129.4; DB 4; Length 1131;
	Best Local Similarity	99.9%; Pred. No. 3e-310;
	Matches 1130; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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Qy	181	AGACAAGCGAAACCTGCCGAGACGAAGGGTTTGGATTTGTAGCTTGCACCTTCAGA 240
Db	181	AGACAAGCGAAACCTGCCGAGACGAAGGGTTTGGATTTGTAGCTTGCACCTTCAGA 240
Qy	241	AACAGTCTGAAGCCTTTAAATGACAGCATCTGCGATGTGAGGAAGGCACCTCCACAGA 300
Db	241	AACAGTCTGAAGCCTTTAAATGACAGCATCTGCGATGTGAGGAAGGCACCTCCACAGA 300
Qy	301	AAACCTCGGATCAATTCTCAGCTGGTGGCAACAACAGTGGCAACAAGTATGCCACCCCA 360
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Qy	361	CCACCCCTTAAAAAGGAGAAAGGAGAAAGTTGAAAGCAGGACAAAGAGAAACCTGAG 420
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Qy	421	AAAGCAAGGAAATTAGTCTTAGTGTTCACGAGAAAAATACCAACAGAAAAACCAACCA 480
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Qy	481	AAAGTCTGACATTTCTGAAGATCTCTTAGTGAACCAACACGATACACAGTCTGCAAAATGCT 540
Db	481	AAAGTCTGACATTTCTGAAGATCTCTCTTAGTGAACCAACGATACACAGTCTGCAAAATGCT 540
Qy	541	ACAACAAGACCCAGCGAAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTGACAGG 600
Db	541	ACAACAAGACCCAGCGAAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTGACAGG 600
Qy	601	AGCATGCAAGCATGTTGGCAGTAATCTGTGGGCAACGTCAACCGTCATTATCACAGACTTT 660
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Qy	661	AAGGAAAGACTTCGCTCTCATCGACATCTCTCATCCAGTGAACCTCCAGTGAAGGCTCA 720
Db	661	AAGGAAAGACTTCGCTCTCATCGACATCTCTCATCCAGTGAACCTCCAGTGAAGGCTCA 720
Qy	721	GAAACAGCAAGACCCAGAGCAGCTCGGGGTACAGAGACACAGAAAGGCTCTCTCCGTTCC 780
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Qy	781	TCCAGGCCAAAGGGGCAATGTACAGCAGTCAATGATGATCTTTGTGAAATTGCACATGG 840
Db	781	TCCAGGCCAAAGGGGCAATGTACAGCAGTCAATGATGATCTTTGTGAAATTGCACATGG 840
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Qy	901	GCATCCCTGGAGAAATCTTCTGTGGAACATCGACCTCTTAGTGATGCTGCAGGATAATTC 960
Db	901	GCATCCCTGGAGAAATCTTCTGTGGAACATCGACCTCTTAGTGATGCTGCAGGATAATTC 960
Qy	961	TGCTTTGCCATGGGCATCTGGGCCACCAAGGAATTTCCGACCCCTGACGATTACTCTTGACAC 1020

CC	of the AAP-1-b cDNA clone encoding a partial AAP-1-b protein	
XX		
SQ	Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other; Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	Query Match 99.9%; Score 1129.4; DB 5; Length 1131; Best Local Similarity 99.9%; Pred. No. 3e-310;	
Db	1 TATTAACCTATCTATTTCGATGATGAAGATACCCCAACCAACCAAAAGAGATCTGGAAT 60	1 TATTAACCTATCTATTTCGATGATGAAGATACCCCAACCAACCAAAAGAGATCTGGAAT 60
Qy	61 TCGATCTCTGAGGCGCAGAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGG 120	61 TCGATCTCTGAGGCGCAGAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGG 120
Db	61 TCGATCTCTGAGGCGCAGAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGG 120	61 TCGATCTCTGAGGCGCAGAGGCTTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGG 120
Qy	121 GGGCGGGGTACAGCCCATCCATGACCATGCGGCACAAAGAGCGCCGACAGGCCAAAA 180	121 GGGCGGGGTACAGCCCATCCATGACCATGCGGCACAAAGAGCGCCGACAGGCCAAAA 180
Db	121 GGGCGGGGTACAGCCCATCCATGACCATGCGGCACAAAGAGCGCCGACAGGCCAAAA 180	121 GGGCGGGGTACAGCCCATCCATGACCATGCGGCACAAAGAGCGCCGACAGGCCAAAA 180
Qy	181 AGACAAGGAAACCTGCGCGAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGA 240	181 AGACAAGGAAACCTGCGCGAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGA 240
Db	181 AGACAAGGAAACCTGCGCGAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGA 240	181 AGACAAGGAAACCTGCGCGAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGA 240
Qy	241 AACAGTGTGAAGCCTTTAAATGACGATCTGCGATGTGAGGAAGGCACTTCCACCAGA 300	241 AACAGTGTGAAGCCTTTAAATGACGATCTGCGATGTGAGGAAGGCACTTCCACCAGA 300
Db	241 AACAGTGTGAAGCCTTTAAATGACGATCTGCGATGTGAGGAAGGCACTTCCACCAGA 300	241 AACAGTGTGAAGCCTTTAAATGACGATCTGCGATGTGAGGAAGGCACTTCCACCAGA 300
Qy	301 AAACCTCGGATCAATTTCTAGCTGGTGCCACAACAAGTGGCACACAGTATGCCACCCCA 360	301 AAACCTCGGATCAATTTCTAGCTGGTGCCACAACAAGTGGCACACAGTATGCCACCCCA 360
Db	301 AAACCTCGGATCAATTTCTAGCTGGTGCCACAACAAGTGGCACACAGTATGCCACCCCA 360	301 AAACCTCGGATCAATTTCTAGCTGGTGCCACAACAAGTGGCACACAGTATGCCACCCCA 360
Qy	361 CCACCCCTTAAAGAGAGAGAGAGAAAGTTGAAAGACGAGCAAGAAACCTTGAG 420	361 CCACCCCTTAAAGAGAGAGAGAGAAAGTTGAAAGACGAGCAAGAAACCTTGAG 420
Db	361 CCACCCCTTAAAGAGAGAGAGAGAAAGTTGAAAGACGAGCAAGAAACCTTGAG 420	361 CCACCCCTTAAAGAGAGAGAGAGAAAGTTGAAAGACGAGCAAGAAACCTTGAG 420
Qy	421 AAAGCAGAGGAAATTTAGTCTTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA 480	421 AAAGCAGAGGAAATTTAGTCTTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA 480
Db	421 AAAGCAGAGGAAATTTAGTCTTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA 480	421 AAAGCAGAGGAAATTTAGTCTTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA 480
Qy	481 AAGTCTGACATTTCTGAAGATTCCTCTAGTGAAGCAACACAGCATACAGTCTGCAATGCT 540	481 AAGTCTGACATTTCTGAAGATTCCTCTAGTGAAGCAACACAGCATACAGTCTGCAATGCT 540
Db	481 AAGTCTGACATTTCTGAAGATTCCTCTAGTGAAGCAACACAGCATACAGTCTGCAATGCT 540	481 AAGTCTGACATTTCTGAAGATTCCTCTAGTGAAGCAACACAGCATACAGTCTGCAATGCT 540
Qy	541 ACAACAAGACCGGCAAAACAAATCACACCTCAAGGCGCCCGGTGAAAAACGTGGACAG 600	541 ACAACAAGACCGGCAAAACAAATCACACCTCAAGGCGCCCGGTGAAAAACGTGGACAG 600
Db	541 ACAACAAGACCGGCAAAACAAATCACACCTCAAGGCGCCCGGTGAAAAACGTGGACAG 600	541 ACAACAAGACCGGCAAAACAAATCACACCTCAAGGCGCCCGGTGAAAAACGTGGACAG 600
Qy	601 AGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTT 660	601 AGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTT 660
Db	601 AGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTT 660	601 AGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACGTCACCGTCATTATCACAGACTTT 660
Qy	661 AAGGAAAGACTCGCTCTCATCGACATCTCTCATCCACAGTGACCTCCAGTGCAGGGTCA 720	661 AAGGAAAGACTCGCTCTCATCGACATCTCTCATCCACAGTGACCTCCAGTGCAGGGTCA 720
Db	661 AAGGAAAGACTCGCTCTCATCGACATCTCTCATCCACAGTGACCTCCAGTGCAGGGTCA 720	661 AAGGAAAGACTCGCTCTCATCGACATCTCTCATCCACAGTGACCTCCAGTGCAGGGTCA 720
Qy	721 GAAACAGAGAACACAGACAGCTCGGGGTGAGAGAGCAGACAAGGGCTCTCCGTTCC 780	721 GAAACAGAGAACACAGACAGCTCGGGGTGAGAGAGCAGACAAGGGCTCTCCGTTCC 780
Db	721 GAAACAGAGAACACAGACAGCTCGGGGTGAGAGAGCAGACAAGGGCTCTCCGTTCC 780	721 GAAACAGAGAACACAGACAGCTCGGGGTGAGAGAGCAGACAAGGGCTCTCCGTTCC 780
Qy	781 TCCAGCCAAAGGCGCAGATGTGAGCAGTCAATCATGAAATCTTTGTCAAAATTCACATGG 840	781 TCCAGCCAAAGGCGCAGATGTGAGCAGTCAATCATGAAATCTTTGTCAAAATTCACATGG 840
Db	781 TCCAGCCAAAGGCGCAGATGTGAGCAGTCAATCATGAAATCTTTGTCAAAATTCACATGG 840	781 TCCAGCCAAAGGCGCAGATGTGAGCAGTCAATCATGAAATCTTTGTCAAAATTCACATGG 840
Qy	841 AATTGTGAAAACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCCATGCTGCTT 900	841 AATTGTGAAAACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCCATGCTGCTT 900
Db	841 AATTGTGAAAACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCCATGCTGCTT 900	841 AATTGTGAAAACTATGAATCAGGGTATGAATTCAAAACCTCCACCTGCCCATGCTGCTT 900
Qy	901 GCATCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGCTGCGAGGATAATTC 960	901 GCATCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGCTGCGAGGATAATTC 960
Db	901 GCATCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGCTGCGAGGATAATTC 960	901 GCATCCCTGGAGAACTTTCTGTGACATCGACCTCTTAGTGATGCTGCGAGGATAATTC 960
Qy	961 TGCTTGCCATGGGCATCTGGGCCACCAAGGAATTTTCGACCCCTGACGATTACTCTTGACAC 1020	961 TGCTTGCCATGGGCATCTGGGCCACCAAGGAATTTTCGACCCCTGACGATTACTCTTGACAC 1020
Db	961 TGCTTGCCATGGGCATCTGGGCCACCAAGGAATTTTCGACCCCTGACGATTACTCTTGACAC 1020	961 TGCTTGCCATGGGCATCTGGGCCACCAAGGAATTTTCGACCCCTGACGATTACTCTTGACAC 1020
Qy	1021 TTTTATGTATTCATTTGTTTATATATATTTTCTTAAATCATTTTATAATTTGATGCT 1080	1021 TTTTATGTATTCATTTGTTTATATATATTTTCTTAAATCATTTTATAATTTGATGCT 1080
Db	1021 TTTTATGTATTCATTTGTTTATATATATTTTCTTAAATCATTTTATAATTTGATGCT 1080	1021 TTTTATGTATTCATTTGTTTATATATATTTTCTTAAATCATTTTATAATTTGATGCT 1080
Qy	1081 CTTGAATCTACTTTTATATAAAGGCTTCGTGGCTTCGAGAGATCTATGA 1131	1081 CTTGAATCTACTTTTATATAAAGGCTTCGTGGCTTCGAGAGATCTATGA 1131
Db	1081 CTTGAATCTACTTTTATATAAAGGCTTCGTGGCTTCGAGAGATCTATGA 1131	1081 CTTGAATCTACTTTTATATAAAGGCTTCGTGGCTTCGAGAGATCTATGA 1131
RESULT 4		
AAZ52452		
ID	AAZ52452 standard; DNA; 3641 BP.	
XX	AAZ52452;	
AC	AC	
XX	XX	
DT	24-FEB-2000 (first entry)	
XX	HTRM clone 3149729 DNA sequence.	
DE	HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS;	
XX	arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; ss;	
KW	Addison's disease; multiple sclerosis; rheumatoid arthritis; infection;	
KW	trauma; myaesthesia gravis; adenocarcinoma; immune disorder; treatment.	
XX		
OS	Homo sapiens.	
XX	XX	
PN	WO9957144-A2.	
XX	XX	
PD	11-NOV-1999.	
XX	XX	
PF	04-MAY-1999; 99WO-US0009935.	
XX	XX	
PR	05-MAY-1998; 98US-0084254P.	
XX	XX	
PR	07-AUG-1998; 98US-0095827P.	
XX	XX	
PR	02-OCT-1998; 98US-0102745P.	
XX	XX	
PA	(INCY-) INCYTE PHARM INC.	
XX	Hillman JL, Bandman O, Lal P, Yue H, Reddy R, Tang YT;	
PI	Gerstin EH, Patterson C, Baughn MR, Azimzai Y, Lu DAM;	
XX	WPI; 2000-052941/04.	
DR	P-PSDB; AAY73367.	
XX	New peptides useful for diagnosis, prevention and treatment of cancer and immune disorders.	
PT	Claim 9; Page 176-177; 193pp; English.	
XX	AAZ52410-252474 are human transcriptional regulator molecule (HTRM) nucleotide sequences. The HTRM protein and nucleotide sequences are useful for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell proliferative disorders such as arteriosclerosis and cirrhosis; cancers including adenocarcinoma and leukaemia; immune disorders such as AIDS, Addison's disease, diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, and myaesthesia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques.	
CC	Polynucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression. Antibodies which specifically bind HTRM and polynucleotides encoding HTRM are useful for diagnosing disorders associated with the expression of HTRM, particularly in assays that detect the expression of HTRM. Nucleotide sequences encoding HTRM may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect	

CC differences in gene sequences among normal, carrier and affected
CC individuals. Using diagnostic assays, cancer can be detected prior to the
CC appearance of clinical symptoms and thereby progression of cancer can be
CC prevented by aggressive treatment or preventive measures
XX
SQ

Sequence 3641 BP; 1081 A; 718 C; 738 G; 1104 T; 0 U; 0 Other;

Query Match 90.3%; Score 1021; DB 3; Length 3641;

Best Local Similarity 99.5%; Pred. No. 3.8e-279; Indels 0; Gaps 0;
Matches 1024; Conservative 0; Mismatches 5;

```
Qy 75 CCACGAAGGCGTTCTCTCCGAGCGCGCGGTTTCGGCTTGGGGGGGGGGGTACAG 134
Db |||
Qy 135 CCATTCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 194
Db |||
Qy 137 CCCATCCATGACATGCGGCGCAAGAGAGAGCCGACAGCCCAAAAGACAGCGAACC 196
Db |||
Qy 195 TGCCGCGAGCAAGGCTTTGGGATTGTAGCGTCTGCACCTTTCAGAAACAGTGTGAAGC 254
Db |||
Qy 197 TGCCGCGAGCAAGGCTTTGGGATTGTAGCGTCTGCACCTTTCAGAAACAGTGTGAAGC 256
Db |||
Qy 255 CTTTAAATGCAGCATCTCGCATGTGAGGAAAGGCACTTCCACAGAAACCTCGGATCAA 314
Db |||
Qy 257 CTTTAAATGCAGCATCTCGCATGTGAGGAAAGGCACTTCCACAGAAACCTCGGATCAA 316
Db |||
Qy 315 TTCTCAGTGTGGGCAAAAGTGGGCAACAGTATGCCACCCGACCCCTTAAAAA 374
Db |||
Qy 317 TTCTCAGTGTGGGCAAAAGTGGGCAACAGTATGCCACCCGACCCCTTAAAAA 376
Db |||
Qy 375 GGAGAGAGAGAGAAAGTTGAAAGAGCAGCAAGAGAAACCTGAGAAAGCAAGGAAAT 434
Db |||
Qy 377 GGAGAGAGAGAGAAAGTTGAAAGAGCAGCAAGAGAAACCTGAGAAAGCAAGGAAAT 436
Db |||
Qy 435 TAGTCCTAGTGTATACCAAGAAAAATACCAAGAAAAACCAAAACCAAGTCTGACATTCT 494
Db |||
Qy 437 TAGTCCTAGTGTATACCAAGAAAAATACCAAGAAAAACCAAAACCAAGTCTGACATTCT 496
Db |||
Qy 495 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAG 554
Db |||
Qy 497 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGCTCAACAAAGACGAG 556
Db |||
Qy 555 CGAAACAAATCACACCTCAAGCCCGCGCTGAAAGAGCAGGAGGACCTGCACAGCA 614
Db |||
Qy 557 CGAAACAAATCACACCTCAAGCCCGCGCTGAAAGAGCAGGAGGACCTGCACAGCA 616
Db |||
Qy 615 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAAGACTCG 674
Db |||
Qy 617 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAAGACTCG 676
Db |||
Qy 675 CTCCTCATCGACATCCTCATCAGTGAACCTTCCAGTGGAGGTCAGAAAGCAGCAACCA 734
Db |||
Qy 677 CTCCTCATCGACATCCTCATCAGTGAACCTTCCAGTGGAGGTCAGAAAGCAGCAACCA 736
Db |||
Qy 735 GAGCAGCTCGGGGTGAGAGAGCAGCAAGAGGCTCCCTCCGTTCTCCAGCCCAAGGG 794
Db |||
Qy 737 GAGCAGCTCGGGGTGAGAGAGCAGCAAGAGGCTCCCTCCGTTCTCCAGCCCAAGGG 796
Db |||
Qy 795 CGACATGTGAGAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGTGAAACTA 854
Db |||
Qy 797 CGACATGTGAGAGTCAATGATGAATCTTTGTGAAATTTGCACATGGAATTTGTGAAACTA 856
Db |||
Qy 855 TGAATCAGGGTATGAAATTTCAAAACCTCCAGTGGGTCAGTGTGATCCCTGGAGAA 914
Db |||
Qy 857 TGAATCAGGGTATGAAATTTCAAAACCTCCAGTGGGTCAGTGTGATCCCTGGAGAA 916
Db |||
Qy 915 TCTTCTGTGGACATCGACCTCTAGTGTGATGCTGCCAGGATATTTCTGCTGCCATGGGC 974
Db |||
Qy 917 TCTTCTGTGGACATCGACCTCTAGTGTGATGCTGCCAGGATATTTCTGCTGCCATGGGC 976
Db |||
Qy 975 ATCTGCGCCCAAGGAAATTTCCGACCTTGACCATTTACTCTTGACACTTTTATGTAATCCA 1034
Db |||
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Db 977 ATCTGCCCAAGGAATTTCCGACCCCTGACGATTAATCTCTTGACACTTTTATGTAATCCA 1036
Qy 1035 TTCTTTATATGATTTTCTCTAAACAATCATTTATAAATGGATGTGCTCTGAAATCTACTTT 1094
Db |||
Qy 1037 TTGTTTATATGATTTTCTCTAAACAATCATTTATAAATGGATGTGCTCTGAAATCTACTTT 1096
Db |||
Qy 1095 TTATAAAAA 1103
Db |||
Qy 1097 TTATAAAAA 1105
Db |||

RESULT 5
ADK66994
ID ADK66994 standard; DNA; 1036 BP.
XX
AC ADK66994;
XX
DT 06-MAY-2004 (first entry)
XX
DE Gene #84 for inhibitory RNA to manipulate stem cell phenotype.
XX
KW ds; gene; inhibitory RNA; RNAi; Notch signaling target gene; phenotype;
XX pluripotent stem cell.
XX
OS Homo sapiens.
XX
PN WO2003068961-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-GB000579.
XX
PR 13-FEB-2002; 2002GB-00003359.
XX
PR 13-FEB-2002; 2002GB-00003387.
XX
PA (AXOR-) AXORDIA LTD.
XX
PI Andrews P, Walsh J, Gokhale P;
XX
XX WPI; 2003-697528/66.
XX
XX New inhibitory RNA molecule having double stranded RNA molecules, useful
XX for manipulating the phenotype of stem cells, preferably pluripotent
XX stem cells.
XX
XX Disclosure; SEQ ID NO 84; 157pp; English.
XX
XX The invention relates to an inhibitory RNA (RNAi) molecule derived from a
XX nucleic acid molecule comprising a defined nucleic acid sequences given
XX in the specification or a sequence which hybridizes to the sequences and
XX encodes a Notch signaling target gene or which is a degenerate as a
XX result of the genetic code of the sequences. The methods and compositions
XX of the present invention are useful for manipulating the phenotype of
XX stem cells, preferably pluripotent stem cells. This sequence corresponds
XX to one of the nucleic acid molecules of the invention.
XX
SQ Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 90.1%; Score 1019.4; DB 10; Length 1036;
Best Local Similarity 99.4%; Pred. No. 5.6e-279; Indels 0; Gaps 0;
Matches 1023; Conservative 0; Mismatches 6;
```

255 CTTTAAATGCAGCATCTCGATGTGAGGAAGGCACCTCCACAGAAAACCTCGATCAA 314
Dd
181 CTTTAAATGCAGCATCTCGATGTGAGGAAGGCACCTCCACAGAAAACCTCGATCAA 240
Qy 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAGTATGCCACCCACCCCTTAAAAA 374
Dd 241 TTCTCAGCTGGTGGCAACAAGTGGCAACAGTATGCCACCCACCCCTTAAAAA 300
Qy 375 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAT 434
Dd 301 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAT 360
Qy 435 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGATCTT 494
Dd 361 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGATCTT 420
Qy 495 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCAG 554
Dd 421 GAAAGATCCTCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCAG 480
Qy 555 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACGTTGGACAGGAGCACTGCACAGCA 614
Dd 481 CGAAACAAATCACACCTCAAGGCCCGGCTGAAAACGTTGGACAGGAGCACTGCACAGCA 540
Qy 615 GTTGGCAGTAACTCTGGGCAAGCTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 674
Dd 541 GTTGGCAGTAACTCTGGGCAAGCTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 600
Qy 675 CTCCTCATCGACATCTCATCCACAGTGACCTCCAGTGCAGGGTCCAGAACAGCAGAACCA 734
Dd 601 CTCCTCATCGACATCTCATCCACAGTGACCTCCAGTGCAGGGTCCAGAACAGCAGAACCA 660
Qy 735 GAGCAGCTCGGGGTGAGAGACACAGCAAGGGCTCTCCCGTTCTCCACGCGCAAGGG 794
Dd 661 GAGCAGCTCGGGGTGAGAGACACAGCAAGGGCTCTCCCGTTCTCCACGCGCAAGGG 720
Qy 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAATTTGCACATGGAAATTTGGAACCTA 854
Dd 721 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAATTTGCACATGGAAATTTGGAACCTA 780
Qy 855 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGGAGAA 914
Dd 781 TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGTGCATCCCTCGGAGAA 840
Qy 915 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCAGGATTAATTTCTGCTTGCATGGGC 974
Dd 841 TCTTCTGTGACATCGACCTCTTAGTGATGCTGCAGGATTAATTTCTGCTTGCATGGGC 900
Qy 975 ATCTGGCCACCAAGGAATTTGGCACCTCGAGATTACTCTTGACATTTTATGATTTCCA 1034
Dd 901 ATCTGGCCACCAAGGAATTTGGCACCTCGAGATTACTCTTGACATTTTATGATTTCCA 960
Qy 1035 TTGTTTTATATGATTTTCTTAAACATCATTTATTAATTTGGATGTGCTCCTGAATCTACTTT 1094
Dd 961 TTGTTTTATATGATTTTCTTAAACATCATTTATTAATTTGGATGTGCTCCTGAATCTACTTT 1020
Qy 1095 TTATAAAAA 1103
Dd 1021 TAATAAAAA 1029

RESULT 6

ADK61399
ID ADK61399 standard; DNA; 1036 BP.

XX AC ADK61399;

XX AC ADK61399;

DT 06-MAY-2004 (first entry)
XX Ovarian cancer-related DNA #554 with altered ovarian cancer expression.
DE ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
XX KW

gene expression; primer; cancer.

Homo sapiens.

WO2003068054-A2.

21-AUG-2003.

13-FEB-2003; 2003WO-US004688.

13-FEB-2002; 2002US-0357031P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

(SLOK) SLOAN KETTERING INST CANCER RES.

Jazaeri AA, Boyd J, Liu ET;

WPI; 2003-689589/65.

Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of several markers.

Disclosure; SEQ ID NO 569; 137pp; English.

The invention relates to a method of classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a pattern of expression in the ovarian tumor of several markers given in the specification; and (2) comparing a similarity of the pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. The method is useful for classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. This sequence corresponds to an ovarian cancer-related gene having an altered pattern of expression in ovarian cancer. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences).

Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;

Query Match 90.1%; Score 1019.4; DB 10; Length 1036;

Best Local Similarity 99.4%; Pred. No. 5.6e-279;

Matches 1023; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 75 CCACGAAGCGCTTCTCTCCGAGCGCGCGCTTTCGGCTTGGGGGGGGGGGTACAG 134

Dd 1 CC CGGAGCGGCTTCTCTCCGAGCGCGCGCTTTCGGCTTGGGGGGGGGGGTACAG 60

Qy 135 CCCATCCATGACCATGGCGACAAAGAGAGCCGACAGGCCAAAAGACAAAGCGAAACC 194

Dd 61 CCATTCATGACCATGGCGACAAAGAGAGCCGACAGGCCAAAAGACAAAGCGAAACC 120

Qy 195 TGCCGAGACGAAAGGGTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTCTGAAGC 254

Dd 121 TGCCGAGACGAAAGGGTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTCTGAAGC 180

Qy 255 CTTTAAATGCAGCATCTGCGATGTGAGGAAGGCACCTCCACAGAAAACCTCGGATCAA 314

Dd 181 CTTTAAATGCAGCATCTGCGATGTGAGGAAGGCACCTCCACAGAAAACCTCGGATCAA 240

Qy 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAAAAA 374

Dd 241 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAAAAA 300

Qy 375 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAT 434

Dd 301 GGAGAAGAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTTGAGAAAGCAAGGAAT 360

Qy 435 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGACATCTT 494

Dd 361 TAGTCTAGTGTATACCAAGAAAATACCAAGAAAACCAAAACCAAGTCTGACATCTT 420

495	QY	GAAGAATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTTACAAACAAGACCAG	554
496			
497			
498			
499			
421	DB	GAAGAATCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTTACAAACAAGACCAG	480
422			
423			
424			
425			
555	QY	CGAAAACAATTCACACCTCAAGGCCCCGGCTGAAAAACGTGACAGGAGCACTGCACAGCA	614
556			
557			
558			
559			
481	DB	CGAAAACAATTCACACCTCAAGGCCCCGGCTGAAAAACGTGACAGGAGCACTGCACAGCA	540
482			
483			
484			
485			
615	QY	GTGGGCAAGTAACTGTGGGCAACGCTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG	674
616			
617			
618			
541	DB	GTGGGCAAGTAACTGTGGGCAACGCTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG	600
542			
543			
544			
675	QY	CTCCTCATGACATCTCTCATCTCAGTGACCTCCAGTGACGGTTCAGAACAGCAGAACCA	734
676			
677			
601	DB	CTCCTCATGACATCTCTCATCTCAGTGACCTCCAGTGACGGTTCAGAACAGCAGAACCA	660
602			
603			
604			
735	QY	GACGAGCTGGGGTTCAGAGAGCACAGACAAGGGCTCCTCCCGTTCTCTCCACGCCAAGGG	794
736			
737			
661	DB	GACGAGCTGGGGTTCAGAGAGCACAGACAAGGGCTCCTCCCGTTCTCTCCACGCCAAGGG	720
662			
663			
664			
795	QY	CGACATGTCAGCAGTCAATGATGAATCTTTGTGAATTCACATGGAAATTTGTGAAAACCTA	854
796			
797			
721	DB	CGACATGTCAGCAGTCAATGATGAATCTTTGTGAATTCACATGGAAATTTGTGAAAACCTA	780
722			
723			
855	QY	TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTTGCACTCCCTGGAGAA	914
856			
857			
781	DB	TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTTGCACTCCCTGGAGAA	840
782			
783			
915	QY	TCCTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAAATTCCTGCTTGCCATGGGC	974
916			
917			
841	DB	TCCTCTGTGACATCGACCTCTTAGTGATGCTGCCAGGATAAATTCCTGCTTGCCATGGGC	900
842			
843			
975	QY	ATCTGGCCACAAGGAATTTTCGACACCTCGACGATTACTCTTTGACACTTTTATGTATTC	1034
976			
977			
901	DB	ATCTGGCCACAAGGAATTTTCGACACCTCGACGATTACTCTTTGACACTTTTATGTATTC	960
902			
903			
1035	QY	TTGTTTATATGATTTTCTTAAACAATCATTTATAATTTGGATGTGCTCCTGAACTACTTT	1094
1036			
961	DB	TTGTTTATATGATTTTCTTAAACAATCATTTATAATTTGGATGTGCTCCTGAACTACTTT	1020
962			
963			
1095	QY	TTATATAAAA 1103	
1096			
1021	DB	TAATAAAAA 1029	
1022			
1023			
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Db 505 GAAAGATCCTCTCTAGTGAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAACAAAGACCAG 564
Qy 555 CGAAACAAATCACACCTCAGGCCCGCGCTGAAACAAAGTGGACAGGAGCATGTCACAGCA 614
Db 565 CGAAACAAATCACACCTCAGGCCCGCGCTGAAACAAAGTGGACAGGAGCATGTCACAGCA 624
Qy 615 GTTGGCAGTAACTGTGGCAACGTCACCGTCATTATCACAGACTTTAAAGGAAAGACTCG 674
Db 625 GTTGGCAGTAACTGTGGCAACGTCACCGTCATTATCACAGACTTTAAAGGAAAGACTCG 684
Qy 675 CTCCTCATCGACATCCTCATCCACAGTGAACCTCCAGTGCAGGGGTGAGAACAGCAGCAACCA 734
Db 685 CTCCTCATCGACATCCTCATCCACAGTGAACCTCCAGTGCAGGGGTGAGAACAGCAGCAACCA 744
Qy 735 GAGCAGCTCGGGGTGAGAGCAGACAGAGGGCTCCTCCGCTTCCTCCAGCGCAAGGG 794
Db 745 GAGCAGCTCGGGGTGAGAGCAGACAGAGGGCTCCTCCGCTTCCTCCAGCGCAAGGG 804
Qy 795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATGACATGGAATTTGGAACACTA 854
Db 805 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATGACATGGAATTTGGAACACTA 864
Qy 855 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTTCGATCCCTCGAGAA 914
Db 865 TGAATCAGGGTATGAAATTTCAAAACCTCCACCTGCCCATGCTGCTTCGATCCCTCGAGAA 924
Qy 915 TCTTCTGTGACATCGACCTCTTAGTGATGTCGACGAGTAATTTCTGCTTGCATGGGC 974
Db 925 TCTTCTGTGACATCGACCTCTTAGTGATGTCGACGAGTAATTTCTGCTTGCATGGGC 984
Qy 975 ATCTGGCCACCAAGGAATTTGCGACCTCGACGATTACTTTGACACATTTTATGATTCCA 1034
Db 985 ATCTGGCCACCAAGGAATTTGCGACCTCGACGATTACTTTGACACATTTTATGATTCCA 1044
Qy 1035 TTGTTTTATGATTTTCTTAACAAATCATTTATTAATTTGGATGCTCCTCGAATCTACTTT 1094
Db 1045 TTGTTTTATGATTTTCTTAACAAATCATTTATTAATTTGGATGCTCCTCGAATCTACTTT 1104
Qy 1095 TTATAAAAA 1103
Db 1105 TTATAAAAA 1113

RESULT 8
ADD18793
ID ADD18793 standard; DNA; 4700 BP.

XX AC ADD18793;
XX DT 15-JAN-2004 (first entry)
XX DE Human disease related protein DNA sequence SeqID224.
XX KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing; gene; ds.
XX OS Homo sapiens.
XX PN WO2003018621-A2.
XX PD 06-MAR-2003.
XX PF 23-AUG-2002; 2002WO-GB003892.
XX PR 23-AUG-2001; 2001GB-00020558.
XX PR 05-OCT-2001; 2001GB-00024037.
XX

PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
PI WPI; 2003-290046/28.
XX P-PSDB; ADD18792.
XX PT New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
XX wound healing.
XX PS Claim 27; SEQ ID NO 224; 424pp; English.
XX CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnery activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX SQ Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;
Query Match 90.0%; Score 1017.8; DB 10; Length 4700;
Best Local Similarity 99.3%; Pred. No. 3.5e-278;
Matches 1022; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 75 CCACGAGGCTTTCTCTCCGAGCGCGCGCTTTTCGGCTTTGGGGGGGGCGGGGTACAG 134
Db 126 CCGGACGCGGTTTCTCTCCGAGCGCGCGCTTTTCGGCTTTGGGGGGGGCGGGGTACAG 185
Qy 135 CCATCCATGACCATGGGGGACAAAGAGCCCGACAGCCCAAAAGACAGCGAAACC 194
Db 186 CCATCCATGACCATGGGGGACAAAGAGCCCGACAGCCCAAAAGACAGCGAAACC 245
Qy 195 TGCCGACAGAGGGTTTGGGATTTGAGCTGCTCAGCTTCAGAAAAGTCTCAGC 254
Db 246 TGCCGACAGAGGGTTTGGGATTTGAGCTGCTCAGCTTCAGAAAAGTCTCAGC 305
Qy 255 CTTTAAATGACGATCTGCGATGTGAGGAAAGGACCTCCACAGAAAACCTCGGATCAA 314
Db 306 CTTTAAATGACGATCTGCGATGTGAGGAAAGGACCTCCACAGAAAACCTCGGATCAA 365
Qy 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAAAAA 374
Db 366 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACCCCTTAAAAA 425
Qy 375 GGRAGAGAGGAGAAAGTTGAAAGCAGGACGAAAGAACCTTGAGAAAGACAGGAAT 434
Db 426 GGAGAGAGAGGAGAAAGTTGAAAGCAGGACGAAAGAACCTTGAGAAAGACAGGAAT 485
Qy 435 TAGTCTCTAGTGTTCACCAAGAAAATACCAACAGAAAACCCAAACCAAAAGTCTGACATTC 494
Db 486 TAGTCTCTAGTGTTCACCAAGAAAATACCAACAGAAAACCCAAACCAAAAGTCTGACATTC 545
Qy 495 GAAAGATCTCTCTAGTGAAGCAAAAGCATACGTCTGCAATGCTACAAACAAAGACCAG 554
Db 546 GAAAGATCTCTCTAGTGAAGCAAAAGCATACGTCTGCAATGCTACAAACAAAGACCAG 605
Qy 555 CGAAACAAATCACACCTCAAGGCCCGCGCTGAAACAAAGTGGACAGGAGCATCTCAGCA 614
Db 606 CGAAACAAATCACACCTCAAGGCCCGCGCTGAAACAAAGTGGACAGGAGCATCTCAGCA 665
Qy 615 GTTGGCAGTAACTGTGGCAACGTCACCGTCAATTATCAGAGCTTTAAGGAAAAGACTCG 674

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Db      666 GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAAGACTCG 725
Qy      675 CTCCTCATCGCATCTCTCATCTCCAGTGAACCTCCAGTGCAGGGTCAGACAGCAGAACCA 734
Db      726 CTCCTCATCGCATCTCTCATCTCCAGTGAACCTCCAGTGCAGGGTCGGAACAGCAGAACCA 785
Qy      735 GAGCAGCTCGGGGTGAGAGCAGACAGACAGAGGGCTCTCCGGTTCCTCCAGCCCAAGGG 794
Db      786 GAGCAGCTCGGGGTGAGAGCAGACAGACAGAGGGCTCTCCGGTTCCTCCAGCCCAAGGG 845
Qy      795 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCGACATGGAATTTGTGAAACTA 854
Db      846 CGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCGACATGGAATTTGTGAAACTA 905
Qy      855 TGAATCAGGGTATGAAATTCAAACCTCCACCTGCCATGCTGCTGCATCCCTGGAGAA 914
Db      906 TGAATCAGGGTATGAAATTCAAACCTCCACCTGCCATGCTGCTGCATCCCTGGAGAA 965
Qy      915 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGC 974
Db      966 TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGC 1025
Qy      975 ATCTGGCCACCAAGAAATTCGACCTCGACGATTAATCTTTGATGATTTTCA 1034
Db      1026 ATCTGGCCACCAAGAAATTCGACCTCGACGATTAATCTTTGATGATTTTCA 1085
Qy      1035 TTGTTTTATATGATTTCTTAACATCAATTTATATTTGATGATGCTCTGATCTACTTTT 1094
Db      1086 TTGTTTTATATGATTTCTTAACATCAATTTATATTTGATGATGCTCTGATCTACTTTT 1145
Qy      1095 TTATAAAAA 1103
Db      1146 TTATAAAAA 1154

RESULT 9
AAS34877
ID AAS34877 standard; cDNA; 2156 BP.
XX AC AAS34877;
XX DT 04-DEC-2001 (first entry)
XX DE cDNA encoding novel human neoplastic disease associated polypeptide #11.
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX OS Homo sapiens.
XX WO20015163-A1.
XX PN 02-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US001358.
XX PF 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0234584P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
```

PR	01-NOV-2000;	2000US-0244617P.	CC	disorders, pulmonary disorders, cardiovascular disorders and renal
PR	08-NOV-2000;	2000US-0246474P.	CC	disorders. The polynucleotide sequences of the invention are also useful
PR	08-NOV-2000;	2000US-0246475P.	CC	in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
PR	08-NOV-2000;	2000US-0246476P.	CC	the novel human neoplastic disease associated polypeptides of the
PR	08-NOV-2000;	2000US-0246477P.	CC	invention. Note: The sequence data for this patent did not form part of
PR	08-NOV-2000;	2000US-0246478P.	CC	the printed specification, but was obtained in electronic format directly
PR	08-NOV-2000;	2000US-0246523P.	CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246524P.	XX	
PR	08-NOV-2000;	2000US-0246525P.	SQ	Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246526P.		
PR	08-NOV-2000;	2000US-0246527P.		
PR	08-NOV-2000;	2000US-0246528P.		
PR	08-NOV-2000;	2000US-0246532P.		
PR	08-NOV-2000;	2000US-0246609P.		
PR	08-NOV-2000;	2000US-0246610P.		
PR	08-NOV-2000;	2000US-0246611P.		
PR	08-NOV-2000;	2000US-0246613P.		
PR	17-NOV-2000;	2000US-0249207P.		
PR	17-NOV-2000;	2000US-0249208P.		
PR	17-NOV-2000;	2000US-0249209P.		
PR	17-NOV-2000;	2000US-0249210P.		
PR	17-NOV-2000;	2000US-0249211P.		
PR	17-NOV-2000;	2000US-0249212P.		
PR	17-NOV-2000;	2000US-0249213P.		
PR	17-NOV-2000;	2000US-0249214P.		
PR	17-NOV-2000;	2000US-0249215P.		
PR	17-NOV-2000;	2000US-0249216P.		
PR	17-NOV-2000;	2000US-0249217P.		
PR	17-NOV-2000;	2000US-0249218P.		
PR	17-NOV-2000;	2000US-0249244P.		
PR	17-NOV-2000;	2000US-0249245P.		
PR	17-NOV-2000;	2000US-0249246P.		
PR	17-NOV-2000;	2000US-0249265P.		
PR	17-NOV-2000;	2000US-0249297P.		
PR	17-NOV-2000;	2000US-0249299P.		
PR	17-NOV-2000;	2000US-0249300P.		
PR	01-DEC-2000;	2000US-0250160P.		
PR	01-DEC-2000;	2000US-0250391P.		
PR	03-DEC-2000;	2000US-0251030P.		
PR	03-DEC-2000;	2000US-0251988P.		
PR	05-DEC-2000;	2000US-0256719P.		
PR	06-DEC-2000;	2000US-0251479P.		
PR	08-DEC-2000;	2000US-0251856P.		
PR	08-DEC-2000;	2000US-0251868P.		
PR	08-DEC-2000;	2000US-0251869P.		
PR	08-DEC-2000;	2000US-0251989P.		
PR	08-DEC-2000;	2000US-0251990P.		
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		
XX	(HUMA-) HUMAN GENOME SCI INC.			
PA	Rosen CA, Barash SC, Ruben SM;			
XX				
PI				
XX				
XX				
DR	WPI; 2001-465558/50.			
DR	P-PSDB; AAU21678.			
XX				
PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to			
PT	diagnose diseases or disorders associated with aberrant expression or			
PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis.			
XX				
XX	Claim 4; SEQ ID NO 121; 687pp; English.			
PS				
XX				
CC	The present invention relates to the isolation of novel human neoplastic			
CC	disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA			
CC	sequences encoding for these polypeptides. The sequences of the invention			
CC	are useful in the diagnosis, treatment, prevention and/or prognosis of			
CC	disorders involving neoplastic disease such as hyperproliferative			
CC	disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem			
CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or			
CC	Hodgkin's lymphoma). The sequences of the invention may also be useful			
CC	for treating other disorders such as neural disorders, immune system			
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal			

CC	disorders, pulmonary disorders, cardiovascular disorders and renal
CC	disorders. The polynucleotide sequences of the invention are also useful
CC	in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
CC	the novel human neoplastic disease associated polypeptides of the
CC	invention. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
	Query Match 82.7%; Score 935.8; DB 4; Length 2156;
	Best Local Similarity 99.2%; Pred. No. 4.9e-255;
	Matches 951; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY	146 CCATGGCGACAAAGAGAGCCCGACAGGCCAAAAGACAAGCGAAACCTGGCGAGCG 205
DB	
	1 CCACGCGTCGAGAGAGAGCCCGACAGGCCAAAAGACAAGCGAAACCTGGCGAGCG 60
QY	206 AAGGGTTTTGGGATTGCTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCA 265
DB	
	61 AAGGGTTTTGGGATTGCTAGCGTCTGCACCTTCAGAAACAGTGTGAAGCCTTTAAATGCA 120
QY	266 GCATCTGCGATGTGAGGAAAGGCACCTCCACCA-GAAAAACCTCGGATCAATTCTCAGCTG 324
DB	
	121 GCATCTGCGATGTGAGGAAAGGCACCTCCACCATGAACCTCGGATCAATTCTCAGCTG 180
QY	325 GTGGCACAACAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAG 384
DB	
	181 GTGGCACAACAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAG 240
QY	385 GAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATTTAGTCTTCTAGT 444
DB	
	241 GAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATTTAGTCTTCTAGT 300
QY	445 GTTACCAAGAAAATAACCAAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCCT 504
DB	
	301 GTTACCAAGAAAATAACCAAGAAAACCAACCAAGTCTGACATTTCTGAAAGATCCT 360
QY	505 CTTAGTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGACCAAGCGGAAACAAAT 564
DB	
	361 CTTAGTGAAGCAAAACAGCATACAGTCTGCAATGTCTACAAAGACCAAGCGGAAACAAAT 420
QY	565 CACACCTCAAGCCCGCGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTA 624
DB	
	421 CACACCTCAAGCCCGCGCTGAAAACGTGGACAGGACACTGCACAGCAGTTGGCAGTA 480
QY	625 ACTGTGGGCAACGTCAACCGTCAATTATCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCG 684
DB	
	481 ACTGTGGGCAACGTCAACCGTCAATTATCACAGACTTTTAAGGAAAAGACTCGCTCCTCATCG 540
QY	685 ACATCCTCATCCACAGTGACCTCCAGTGAGGGTCAAGAACAGGAGAACCCAGAGCAGCTCG 744
DB	
	541 ACATCCTCATCCACAGTGACCTCCAGTGAGGGTCAAGAACAGGAGAACCCAGAGCAGCTCG 600
QY	745 GGGTCAGAGCAGACAGCAAGGGCTCTCCCGTCTCTCCACGCCAAGCGGCACATGTCA 804
DB	
	601 GGGTCAGAGCAGACAGCAAGGGCTCTCTCCCGTCTCTCCACGCCAAGCGGCACATGTCA 660
QY	805 GCAGTCAATGATCAATCTTTTGTGAAATTCACATAGGAATTTGTGAAACATATGAATCAGGG 864
DB	
	661 GCAGTCAATGATCAATCTTTTGTGAAATTCACATAGGAATTTGTGAAACATATGAATCAGGG 720
QY	865 TATGAAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCTCCCTGAGAAATCTTCTGTGG 924
DB	
	721 TATGAAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCTCCCTGAGAAATCTTCTGTGG 780
QY	925 ACATGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGCCTCTGSCCAC 984
DB	
	781 ACATGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGCCTCTGSCCAC 840
QY	985 CAAGGAAATTCGACCCCTGACGATTAATCTTGCACACTTTTATGATTCATCTGTTTATA 1044
DB	
	841 CAAGGAAATTCGACCCCTGACGATTAATCTTGCACACTTTTATGATTCATCTGTTTATA 900

[illegible]

XX WO200116165-A2.
PN 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-NL000612.
XX
XX 02-SEP-1999; 99EP-00202858.
PR 21-OCT-1999; 99EP-00203465.
XX
XX (LEAD-) LEADD BV.
XX
XX Noteborn MHM, Danen-Van Oorschot AAAM;
PI WPI; 2001-235090/24.
XX
XX New nucleic acids encoding apoptin-associating proteins useful for
PT inducing apoptosis, particularly p53 independent apoptosis, or for
PT treating cancers or autoimmune diseases.
XX
XX Claim 6; Fig 1; 50pp; English.
XX
XX The present sequence encodes a human apoptin-associating protein 1
CC (AAP1). The protein is capable of providing apoptosis. AAP polypeptides
CC and polynucleotides are useful for inducing apoptosis, particularly when
CC apoptosis is p53-independent. They may be used to produce pharmaceutical
CC compositions which are used for treating a disease where enhanced cell
CC proliferation or decreased cell death is observed, particularly in cancer
CC or in autoimmune diseases, for diagnosing a disease related with
CC aberrancies in the apoptotic process, and for detecting the presence of
CC cancer cells or cells that are prone to cancer
XX
XX Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;
SQ

Query Match 77.9%; Score 881.4; DB 4; Length 947;
Best Local Similarity 97.6%; Pred. No. 9.4e-240;
Matches 902; Conservative 2; Mismatches 19; Indels 1; Gaps 1;
XX 209 GGTTTTGGGATTGAGCGTCTGACCTTCAGAACAGTGTGAGCCCTTTAAATGCAGCA 268
DB 24 GGAATTCGGATCTCTCGAGGCCAGGAGCGCGAAACAGTGTGAGCCCTTTAAATGCAGCA 83
XX 269 TCTCGGATGTGAGGAAGGACCTCCACAGAAACCTCGGATCAATTTCTCAGCTGTGG 328
DB 84 TCTCGGATGTGAGGAAGGACCTCCACAGAAACCTCGGATCAATTTCTCAGCTGTGG 143
XX 329 CACAACAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAGAGA 388
DB 144 CNCAACAAGTGGCACAACAGTATGCCACCCCAACCCCTTAAAGAGAGAGAGAGA 203
XX 389 AAGTTGAAAGCAGGACAGAGAAACCTGAGGAAGACAGGAATTTAGTCTAGTGTGA 448
DB 204 AAGTTGAAAGCAGGACAGAGAAACCTGAGGAAGACAGGAATTTAGTCTAGTGTGA 263
XX 449 CCAAGAAAATACCAACAGAAACCAACCAAGTCTGACATTTCTGAAAGATCCTCCTA 508
DB 264 CCAAGAAAATACCAACAGAAACCAACCAAGTCTGACATTTCTGAAAGATCCTCCTA 323
XX 509 GTGAAGCAACACAGCATACAGTCTGCAATGCTTACAACAGAGACAGGCGAAACAAATCA 568
DB 324 GTGAAGCAACACAGCATACAGTCTGCAATGCTTACAACAGAGACAGGCGAAACAAATCA 383
XX 569 CCTCAGGCCCGGCTGAAAAACGTGAGCAGGAGCAGTGCACAGCAGTTGGCAGTAAGT 628
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XX 629 TGGGCAACGTCCAGTCTATATCAGACTTTAAGGAAAGACCTCGCTCTCATCGCAT 688
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XX 689 CCTCATCAGTGCAGCTCCAGTGCAGGGTTCAGAACAGCAGAGACAGCAGCTCGGGGT 748
DB 504 CCTCATCAGTGCAGCTCCAGTGCAGGGTTCAGAACAGCAGAGACAGCAGCTCGGGGT 563

QY 749 CAGAGAGCAGACAGAGGGCTCTCCCGTTCTCCAGCGCAAGGCGGACATGTCAGCAG 808
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QY 809 TCAATGATGAATCTTTGTGAAAATTGCACATGGAATTTGTGAACATGATCAGGCTATG 868
DB 624 TCAATGATGAATCTTTGTGAAAATTGCACATGGAATTTGTGAACATGATCAGGCTATG 683
QY 869 AAATTCAAAACCTCCACCTGCCCATCTGCTGTCATCCCTCGGAGAAATCTTCTGTGGACAT 928
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QY 929 CGACCTCTTTAGTGATGCTGCCAGGATAATTTCTGCTTGCATGGGCAATCTGTGGCAACAG 988
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QY 1108 TTCTGTGGCCTCGAGAGATCTATGA 1131
DB 924 TTCTGTGGCCTCGAGAGATCTATGA 947

RESULT 12
AAF55404
ID AAF55404 standard; DNA; 947 BP.
XX AC AAF55404;
XX DT 29-MAY-2001 (first entry)
XX DE Nucleotide sequence of an apoptin-associating protein.
XX KW Apoptin-associating proteinaceous substance; cell proliferation;
XX KW apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer;
XX OS Homo sapiens.
FH Key Location/Qualifiers
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FT CDS 96..311
FT /*tag= b
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FT /note= "Xaa is an unspecified residue; encodes AAB67553"
FT CDS 312..401
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FT CDS 519..884
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FT CDS 885..920
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XX
PN
XX EPI081226-A1.

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Qy 255 CTTTAAATGAGCATCTGCGA-TGTGAGGAAGGCACTCCACAGAAACCTCGGATCA 313
Db 184 CTTTAAATGAGCATCTGCGA-TGTGAGGAAGGCACTCCACAGAAACCTCGGATCA 243
Qy 314 ATTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAATA 373
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Qy 428 AGGAATTTAGTCTCT--AGTGTACCAAGAAATACCAACAAGAAACCAACCAAGTC 485
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Qy 486 TGA-CATTCTGAAGATCTCTCTAG-TGAAGCAAAACAGCATACAGTCTGCAAAATGCTACA 543
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Qy 544 ACAAGACCGAGCAAAACATACACC-TCNAGGCCCGGCTGAATAA---CGTGAACAG 599
Db 484 ACAAGACCGAGCAAAACATACACCCTTCAAGGCCCGGCTGAATAA---CGTGAACAG 543
Qy 600 GAGCATCTGACAGCAGTTGG---CAGTAATCTGGGCAACGTCACCGTCAATATACAG 655
Db 544 GGGCATTTGACAGCAGTTTGGGCAAGTTAACTGTGGGGCAACGTCACCGTCAATATACAG 603
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Db 604 ACTTTAAGGAAAGACTCGCTCTCATCGACATCTCATCCACAGTGACCTCCAGTG 663
Qy 713 CAGGCTCA-GAACAGCAGAACCCAG-----AGCAGTCTGGGGTTCAGAG--AGCAGACAG 765
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Qy 766 GGCTCC--TCCGTTCTCC--ACGCCAAGGGCGAC--ATGTCAGCAGTCAATGATGAA 819
Db 724 GGCTCCCTCCCGTTCTCTCCAAACCCCAAGGGGACCATGTCAAGCAGTCAATGATGAA 783
Qy 820 TCTTTGTGAATTT---GCACATGGAATTTGAAACCTATGAA---TCAGGGTATGAAA- 871
Db 784 TCTTTCTGAAATTTGGCAGCATGGGAATTTGGAACCTATGGAATTCAGGGGTATGAAA 843
Qy 872 --TTCAAAACCTCACCCTGGCCATGC-TGCTTGATCCCTGGAGAAATCTTCTGT---GG 924
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Qy 925 ACATCGACCTCTT---AGTGATGCTGCCAGGATATTTCT--GCTTGCATGGGCAAT--C 977
Db 904 ACATCGACCTCTTTAGTTGATTTGCTGCAGATATTTCTTTGCTTTGCCATGGGCAATCT 963
Qy 978 TGGCCAGCAAGGAATTT--CGCACCTCGAGATTTACTCTTGACACTTTT-ATGTAATCCA 1034
Db 964 TGGCCACCAAGGATTTTTCGCACCTCGACGATTTACTCTGGACACTTTTAAATGTAATCCA 1023
Qy 1035 TTGTTTTATATGATTTTCTTAACATCATTTATTAATTTGGATGTGCTCTGAATCTACTTTT 1094
Db 1024 TTGTTTTATATGATTTTCTTAACATCATTTATAATTTGGATGTGCTCTGAATCTACTTTT 1083
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RESULT 15
ACH37647

ID XX ACH37647 standard; cDNA; 502 BP.
AC XX ACH37647;
DT XX 13-OCT-2003 (first entry)
XX Human endothelial cell cDNA #5780.
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
OS Homo sapiens.
PN US2003073623-A1.
XX 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
PS Claim 1; SEQ ID NO 24859; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623
XX Sequence 502 BP; 138 A; 140 C; 118 G; 105 T; 0 U; 1 Other;

Query Match 41.4%; Score 468.4; DB 9; Length 502;
Best Local Similarity 96.6%; Pred. No. 2e-122;
Matches 478; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 522 CATACAGTCTGCAATGCTTACACAAAGACCAGCGAAACAAATCACACCTCAAGGCCCG 581
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Qy 582 GCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACCTCAC 641
Db 68 GCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACCTGTGGCAACCTCAC 127
Qy 642 CGTCATTATCACAGACTTTTAAGGAAAGACTCGCTCCTCATCGACATCTCATCCACAGT 701
Db 128 CGTCATTATCACAGACTTTTAAGGAAAGACTCGCTCCTCATCGACATCTCATCCACAGT 187

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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 188 GACCTCCAGTGCAGGGTCAGAAACAGCAGAACCCAGAGCAGCTCGGGGTACAGAGACACAGA 247
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 762 CAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTACAGCAGTCAATGATGAATC 821
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 248 CAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTACAGCAGTCAATGATGAATC 307
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 822 TTTCTGAAATTGCACATGGAATTGTGAAACTATGAACTCAGGGTATGAAATTCAAAACCT 881
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 308 TTTCTGAAATTGCACATGGAATTGTGAAACTATGAACTCAGGGTATGAAATTCAAAACCT 367
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 882 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAACTTCTGTGGACATCGACCTCTTAGTG 941
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 368 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAACTTCTGTGGACATCGACCTCTTAGTG 427
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Qy 942 ATGCTGCCAGGATAATTCTGCTTGGCCATGGGCATCTGGCCACCAAGGAATTCGCACCC 1001
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Qy 1002 TGACGATTACTCTTG 1016
Db |||||||||||||||||||
Qy 488 TGACGATTACTCTTG 502
Db |||||||||||||||||||
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Job time : 697.404 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 07:52:31 ; Search time 4310.65 Seconds
(without alignments)
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Perfect score: 1131
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	862.2	76.2	895	CK230944	ILLUMIGEN
2	855.4	75.6	1436	AK033024	Mus muscu
3	826.8	73.1	932	AJ816315	AJ816315
C 4	726.2	64.2	799	CK774847	CK774847 963641 MA
C 5	708.6	62.7	736	BM985193	BM985193 UT-CF-EC1
6	691.4	61.1	906	BI553612	603190533
7	672.6	59.5	936	BE300021	600944142
8	671.8	59.4	707	EX924636	EX924636 BX924636
9	668.6	59.1	798	BU704183	BU704183 UI-M-F00-
10	659.2	58.3	870	BG827273	BG827273 602749436
C 11	656.4	58.0	726	CK777039	CK777039 964031 MA
C 12	652.4	57.7	654	AY400131	AY400131 Homo sapi
C 13	645.2	57.0	662	BQ015219	BQ015219 UI-H-ED1-
C 14	634	56.1	664	CK299391	CK299391 UI-E-EJ1-
15	628	55.5	650	BQ189224	BQ189224 UI-E-EJ1-
C 16	616.4	54.5	642	BF116048	BF116048 7n76908.x
C 17	612	54.1	621	AI627241	AI627241 ty72a11.x
18	607.6	53.7	1074	BQ053013	BQ053013 AGENCOURT
19	605.2	53.7	1077	BI114501	BI114501 602862192
20	607.6	53.5	792	CN533672	CN533672 UI-M-H00-
21	603.8	53.4	718	CK636066	CK636066 UI-M-HNO-
22	603.2	53.3	784	CK635466	CK635466 UI-M-HNO-
23	591.4	52.3	769	CA324092	CA324092 UI-M-FY0-
24	588.4	52.0	948	CG494853	CG494853 OST33953

25	583.6	51.6	654	9	AY400133	AY400133 Mus muscu
26	583.6	51.6	751	6	CB724087	CB724087 UI-M-FY0-
27	578.4	51.1	745	6	CD355761	CD355761 UI-M-FY0-
28	577	51.0	639	6	CB444669	CB444669 695860 MA
C 29	574	50.8	618	4	BM312863	BM312863 i980c01.x
30	572.8	50.6	723	7	CN457401	CN457401 UI-M-HNO-
31	569.6	50.4	608	4	BI345349	BI345349 374146 MA
C 32	569.4	50.3	573	1	AI693196	AI693196 wd68f05.x
33	568.4	50.3	610	6	CB287220	CB287220 CMD55_C02
C 34	549.8	48.6	573	1	AI912660	AI912660 wd12c06.x
35	549	48.5	589	6	CB287224	CB287224 CMD55_C09
C 36	548.8	48.5	589	6	CB461283	CB461283 721237 MA
C 37	545.4	48.2	548	2	AW193683	AW193683 xm23d02.x
C 38	544.4	48.1	576	1	AI693651	AI693651 wd79f12.x
C 39	543.4	48.0	564	6	CB854840	CB854840 UI-CF-EC1
40	541.4	47.9	703	7	CK639892	CK639892 UI-M-HNO-
41	541.4	47.9	703	7	CN526226	CN526226 UI-M-HNO-
42	540	47.7	814	9	CG498682	CG498682 OST40156
43	539.4	47.7	700	7	CK640200	CK640200 UI-M-HNO-
C 44	538	47.6	547	1	AA725613	AA725613 a119d09.8
45	537	47.5	545	7	CV029042	CV029042 7711 Full

ALIGNMENTS

RESULT 1
CK230944
LOCUS ILLUMIGEN MCQ_1331 Katze MML2 Macaca mulatta cDNA 5' similar to human RYBP (Hs_7910), mRNA sequence.
DEFINITION CK230944.1 GI:39637302
ACCESSION CK230944
VERSION
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
REFERENCE 1 (bases 1 to 895)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biociences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.10.17, 765 Q20 bases. Assemblies in contig w/ 1 member(s). Contig contains 1 (0%) lib members.
PCR Primers
FORWARD: CCTCTACTAAGGGACAAAA
BACKWARD: CACTATAGGGCGAATTGGTA
Insert Length: 895 Std Error: 0.00
Plate: CL000013 row: C column: 06
Seq primer: CCTCTACTAAGGGACAAAA
POLYA=Yes.

FEATURES

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/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze MML2"
/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: ECOR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-cDNA Gigapack III Gold Cloning Kit (Catalog #200450)"

ORIGIN

Query Match	76.2%;	Score	862.2;	DB	7;	Length	895;
Best Local Similarity	99.1%;	Pred.	No. 1.8e-223;				
Matches	867;	Conservative	0;	Mismatches	22;	Indels	0;
Gaps	0;						
Qy	229	TGCACCTTCAGAAAACAGTCTGTAAGCCCTTTAAATGTCAGCATCTGGATGTGAGGAAAGGC	288				
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Qy	289	ACCTCCACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCAACAACAGTGGCAACAACAG	348				
Db	61	ACCTCCACCAGAAAACCTCGGATCAATTTCTCAGCTGGTGGCAACAACAGTGGCAACAACAG	120				
Qy	349	TATGCCACCCACACCCCTTAAAGAGAGAAAGAGAAAGTGAAGAACGACGACAAA	408				
Db	121	TATGCCACCCACACCCCTTAAAGAGAGAAAGAGAAAGTGAAGAACGACGACAAA	180				
Qy	409	GAGAACTCTGAGAAAGACAGGAATTTAGTCTCTAGTGTTCACAGAAAATACCAACAAG	468				
Db	181	GAGAACTCTGAGAAAGACAGGAATTTAGTCTCTAGTGTTCACAGAAAATACCAACAAG	240				
Qy	469	AAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAG	528				
Db	241	AAAAACCAACCAAGTCTGACATTTCTGAAAGATCTCTCTAGTGAAGCAAAACAGCATACAG	300				
Qy	529	TCTGCAATGCTACAAACAGACAGCAACAAATACACCTCAAGGCCCGGCTGAAA	588				
Db	301	TCTGCAATGCTACAAACAGACAGCAACAAATACACCTCAAGGCCCGGCTGAAA	360				
Qy	599	AACGTGGACAGGACACTGCACAGCAGTTGGCAGTAAGTGTGGGCAACGTCACCGTCAAT	648				
Db	361	AACGTGGACAGGACACTGCACAGCAGTTGGCAGTAAGTGTGGGCAACGTCACCGTCAAT	420				
Qy	649	ATCACAGACTTTAAGGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGAACCTCC	708				
Db	421	ATCACAGACTTTAAGGAAAAGACTCGCTCTCATCGACATCTCTATCCACAGTGAACCTCC	480				
Qy	709	AGTCAGGTCAGACAGCAGACAGCAGCTCGGGTCAGAGCAGCAGACAGAGGC	768				
Db	481	AGTCAGGTCAGACAGCAGACAGCAGCTCGGGTCAGAGCAGCAGACAGAGGC	540				
Qy	769	TCCTCCCGTCTCCACGCAAGGGGACATGTCCAGCAGTCAATGATGAATCTTTGTGA	828				
Db	541	TCCTCCCGTCTCCACGCAAGGGGACATGTCCAGCAGTCAATGATGAATCTTTGTGA	600				
Qy	829	AATTCACATGAATTTGTGAAAACATGATGAATCAGGGTATGAAATTCAAAACCTCCACCTG	888				
Db	601	AATTCACATGAATTTGTGAAAACATGATGAATCAGGGTATGAAATTCAAAACCTCCACCTG	660				
Qy	889	CCATGCTGCTTGCAATCCCTGGAGAACTCTCTGTGGACATCGACCTCTAGTGATGCTGC	948				
Db	661	CCATGCTGCTTGCAATCCCTGGAGAACTCTCTGTGGACATCGACCTCTAGTGATGCTGC	720				
Qy	949	CAGGATAATTTCTGCTTGCCATGCGCATCTGGCCACCAAGGAATTTCCGACCCCTGACGAT	1008				
Db	721	CAGGATAATTTCTGCTTGCCATGCGCATCTGGCCACCAAGGAATTTCCGACCCCTGACGAT	780				
Qy	1009	TACTCTTGACACTTTTATGTAATTCATGTTTATATGATTTTCTTAACAATCAATTTATA	1068				
Db	781	TACTCTTGACACTTTTATGTAATTCATGTTTATATGATTTTCTTAACAATCAATTTATA	840				
Qy	1069	ATTGATGTGCTCTGCAATCTACTTTTTTATAAAAA	1103				
Db	841	AATGATGTGCTCTGCAATCTACTTTTTTATAAAAA	875				

RESULT 2
AK033024
LOCUS
DEFINITION
Mus musculus 11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:703040SH07 product:RING1 and YY1 binding protein, full insert sequence.
AK033024

AK033024.1 GI:26328784
HTC; CAP trapper.
Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1436)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES	Location/Qualifiers	
source	1. .1436	
	/organism="Mus musculus"	
	/mol_type="mRNA"	
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	/dev_stage="11 days embryo"	
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	Best Local Similarity 91.6%; Pred. No.1.4e-221;	
	Matches 939; Conservative 0; Mismatches 81; Indels 5; Gaps 3;	
QY	79 GAAGGCTTCTCTCCGAGCGCGCGTTCGCGCTTGGGGGGGGCGGGTACAGCCCA	138
DB	58 GACCGCGCTTCTCTCTGAGCGCGCGCGCGAGCTGTGGGGCGCGGGCGAGCCG	117
QY	139 TCCATGACCATGGCGGACAAAGAGAGCCGACAGGCCCAAAAGAACAAAGCGAA	198
DB	118 TCCATGACCATGGCGGACAAAGAGAGCCGACAGGCCCAAAAGAACAAAGCGAA	177
QY	199 GCAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTCAGAAACAGTGTGAGCC	258
DB	178 GCAGAGCAAGGGTTTGGGATTTAGCGTCTGCACCTTTAGGAAACAGCGCCGAG	237
QY	259 AATGACGATCTCGCATGTGAGGAAGGACCTCCACAGAAACCTTCGATCAAT	318
DB	238 AATGACGATCTCGCATGTGAGGAAGGACCTCCACAGAAACCTTCGATCAAT	297
QY	319 CAGCTGTGACCAACAAAGTGGCAACAGTATGCGACCCACACCCCTTAAAGAG	378
DB	298 CAGCTGTGACCAACAGTGTGGCAACAGTATGCGACCTCCACCTTAAAGAG	357
QY	379 AAGAGGAGAAAGTTGAAAGACGAGCAAAAGAGAACTTCGAGAAAGCAAGAA	438
DB	358 AAGAGGAGAAAGTTGAAAGACGAGCAAAAGAGAACTTCGAGAAAGCAAGAA	417
QY	439 CTTAGTTTACCAAGAAATATACACAGAAACCAACACCAAGTCTGACATCTG	498
DB	418 CCCAGTGTCCCAAGAAATATACACAGAAACCAACACCAAGTCTGATATCTG	477
QY	499 GATCCTCTAGTGAAGCAACAGCATACAGTCTGCAATGTCTACACAAAGACCA	558
DB	478 GATCCTCTAGTGAAGCAACAGCATACAGTCTGCTAAGCTTACAAAGACCA	537
QY	559 ACAATATCACACCTCAAGGCCCGCGCTGAAAGACGTGGACAGGACCTGCAC	618
DB	538 ACAATATCACACCTCAAGGCCCGCGCTGAAAGACGTGGACAGGACCTGCAC	597
QY	619 GCAGTAATCTGTGGCAACGTCACCGTCATTATACAGACTTAAAGAAAGCTGC	678
DB	598 GCAGTAATCTGTGGCAACGTCACCGTCATTATACAGACTTAAAGAAAGCTGC	657

ORIGIN	(Sahiwal) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"									
	Query Match	73.1%;	Score	826.8;	DB	1;	Length	932;		
	Best Local Similarity	95.2%;	Pred. No.	8e-214;						
	Matches	874;	Conservative	0;	Mismatches	42;	Indels	2;	Gaps	2;
QY	187	GGAAACCTGCCGACAGCAAGGGTTTGGGATTTAGCGTCTGACACTTCAGAAACAGT	246							
Db	1	GCAAAACCTGCCGACAGCAAGAGCTTTTGGGATTTAGCGTCTGCACTTCAGAAAACGC	60							
QY	247	GCTGAAGCCCTTTAAATGTCAGCATCTCGATGTGAGGAAAGGCACCTCCACAGAAAACCT	306							
Db	61	GCGAAGCCCTTTAAATGTCAGTATCTCGATGTGAGAAAGGCACCTCCACAGAAAACCT	120							
QY	307	CGGATCAATTTCTCAGCTGGTGCCACAAAGTGGCACAACAGTATGCCACCCACCAACC	366							
Db	121	CGGATCAATTTCCAGCTGGTGCCACAGCAAGTGGCCAGCAGTATGCTCACTCCACCAACC	180							
QY	367	CCTAAAAGGAGAGAGCAAGTGTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGAC	426							
Db	181	CCTAAAAGGAGAGAGGAGAAAGTTGAAAAACAAGACAAAGAGAAACCTGAGAAAGAT	240							
QY	427	RAGGAAATTTAGTCTTAGTGTTACCAAGAAAAATACCAACAAAGAAAAACCAACCAAGTCT	486							
Db	241	AAAGAAATTTAGTCTTAGTGTTCACCGAGAAAAATACCAACAAAGAAAAACCAACCAAGTCT	300							
QY	487	GACATTTGAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAACA	546							
Db	301	GATATTTCTGAAGATCTCTCTAGCGAAGTGAACAGTATACAGTCTGCAAAATGCTACAACA	360							
QY	547	RAGACCAGGAAACAAATACACCTCAAGSCCCGCTGAAAAACGTGGACAGGAGCACT	606							
Db	361	RAGACCAGTGAACCAATACACCTCAAGSCCCGCTGAAAAACGTGGACAGGAGCAACC	420							
QY	607	GCACAGCAGTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAA	666							
Db	421	GCACAGCAGTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAA	480							
QY	667	RAGACTCGCTCTCATCGACATCTTCATCCAGATGACCTCCAGTGCAGGGTCAGAACAG	726							
Db	481	RAGACTCGCTCTCTCGACATCTTCATCCAGTGAACCTCCAGTGCAGGGTCAGAACAG	540							
QY	727	CAGAACACAGCAGCTCGGGGTGACAGAGACAGCAAGAGGGCTCTCCCGCTTCTCCACG	786							
Db	541	CAGAACACAGCAGCTCGGGGTGAGAGACACAGAGGGTTCCTCCGCTCTCTCCACG	600							
QY	787	CCAAAGGGCGACATGTCAGCAGTCAATGATGAATCTTTGTGAAATTCGACATGGAAATGT	846							
Db	601	CCAAAGGGCGACATGTCAGCAGTAAATGATGAGTCTTTCTGAAATTCGACATGGAAATGT	660							
QY	847	GAAACTATGAATCAGGGTATGAAATTCAAAAACCTCCACTGCCCATCTGCTTGCA-TC	905							
Db	661	GAAACTATGAATCAGGGTATGAAATTCAGTCTCACTGCCCATCTGCTTGCAACC	720							
QY	906	CCTGGAGAAATCTTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTT	965							
Db	721	CCTGGAGAAATCTTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTT	780							
QY	966	GCCATGGGCACTTGGCCACCAAGGAATTTCCGACCTCGACGATTAATCTTGACACTTTTA	1025							
Db	781	GCCATGGGCACTTGGCCACCAAGGAATTTCCGACCTCGACGATTAATCTTGACACTTTTA	840							
QY	1026	TGTAATTCATGTTTTATATGATTTTCTTAAACAAATCATTTATAATGGATGTCCTCTGA	1085							
Db	841	TGTAATTCATGTTTTATATGATTTTCTTAAAC-ATCATTTATAATGGATGTCCTCTGA	899							
QY	1086	ATCTACTTTTTATAAAAA	1103							
Db	900	ATCTACTTTTTATAAAAA	917							

RESULT 4									
CK774847/c	CK774847	799 bp	mrna	linear	EST	20-FEB-2004			
LOCUS	963641 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.								
DEFINITION	CK774847								
ACCESSION	CK774847								
VERSION	CK774847.1 GI:42728990								
KEYWORDS	EST.								
SOURCE	Bos taurus (cow)								
ORGANISM	Bos taurus								
REFERENCE	1 (bases 1 to 799)								
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.								
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle								
JOURNAL	Genome Res. 11 (4), 626-630 (2001)								
MEDLINE	21180013								
PUBMED	11282978								
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: 105 row: P column: 12 Seq primer: GTAATACGACTCACTATAGG. Location/Qualifiers								
FEATURES	1..799								
source	/organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 2BOV" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."								
ORIGIN	Query Match 64.2%; Score 726.2; DB 7; Length 799; Best Local Similarity 95.1%; Pred. No. 2e-186; Matches 760; Conservative 0; Mismatches 38; Indels 1; Gaps 1;								
QY	301	AAACCTCGATCAATTTCTCAGCTGGTGCAACAAGTGGCAACAGTATGCCACCCCA	360						
Db	799	AAACCTCGATCAATTTCCAGCTGGTGCAACAGTGGCCAGCATGTGCCACTCCA	740						
QY	361	CCACCCCTTAAAGAGGAGAGAAAGTTTCAAGAGCAGGACCAAGAACTTGAG	420						
Db	739	CCACCCCTTAAAGAGGAGAGAAAGTTTGAAGAAACAGACAAAGAAACCTGAG	680						
QY	421	AAAGCAAGGAAATTTAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA	480						
Db	679	AAAGATAAGAAATTTAGTCTCTAGTGTACCAAGAAAAATACCAAGAAAAACCAACCA	620						
QY	481	AAGTCTGACATTTGAAAGATCCTCCTAGTGAAGCAACAGCATACAGTCTGCAAAATGCT	540						
Db	619	AAGTCTGATATTTCTGAAGATCCTCCTAGCGAAGTGAACAGTATACAGTCTGCAAAATGCT	560						
QY	541	ACAACAAGACCAAGGAAACAAATCACACCTCAAGGCCCGGCTGAAACAACTGGACAGG	600						
Db	559	ACAACAAGACCAAGTGAACGAATCACACCTCAAGGCCCGGCTGAAACAACTGGACAGG	500						
QY	601	AGCACTGCACAGCTTGGCAGTAACTGTGGGCAACGTCACCGTCAATTATTCACAGACTTT	660						

FEATURES		Location/Qualifiers	
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		/db_xref="taxon:9606"	
		/clones="UI-CF-EC1-acc-m-16-0-UI"	
		/tissue_type="Lung"	
		/dev_stage="Adult and Fetal"	
		/lab_host="DH10B (Life Technologies) (T1 phage resistant)"	
		/clone_lib="UI-CF-EC1"	
		/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGTTCAC."	
		TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383	
		TAG_LIB=UI-CF-EC1	
		TAG_SEQ=AAGTGTTCAC"	
ORIGIN		Query Match 62.7%; Score 708.6; DB 5; Length 736;	
		Best Local Similarity 99.4%; Pred. No. 1.2e-181;	
		Matches 711; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	389	AAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAGACAGAGAAATTAGTCTTAGTGTTA	448
Db	726	AAAGTGAAGCAGGACAAAGAGAAAACCTTGAGAAAGACAGAGAAATTAGTCTTAGTGTTA	667
QY	449	CCAGAGAAATACCAACAGAGAAACCAACCAAGTCTGACATTCGAAAGATCTCTCTA	508
Db	666	CCAAGAAAATACCAACAGAGAAACCAACCAAGTCTGACATTCGAAAGATCTCTCTA	607
QY	509	GTGAAGCAACAGACATACAGTCTGCAATGCTCAACAAGACAGCAGCAACAAATCACA	568
Db	606	GTGAAGCAACAGACATACAGTCTGCAATGCTCAACAAGACAGCAGCAACAAATCACA	547
QY	569	CCTCAAGCCCGCGCTGAAAAACGTGGACAGGACCTGCAAGCAGTGGCAGTAACCTG	628
Db	546	CCTCAAGCCCGCGCTGAAAAACGTGGACAGGACCTGCAAGCAGTGGCAGTAACCTG	487
QY	629	TGGGCAACGTCAACCGTCAATATCAGAGCTTTAGGAAAGACCTGCTCCTCATCGACAT	688
Db	486	TGGGCAACGTCAACCGTCAATATCAGAGCTTTAGGAAAGACCTGCTCCTCATCGACAT	427
QY	689	CCTCATCAGTACCTCAGTGCAGGCTCAGAACAGCAGAACAGCAGCAGCTCGGGGT	748
Db	426	CCTCATCAGTACCTCAGTGCAGGCTCAGAACAGCAGAACAGCAGCAGCTCGGGGT	367
QY	749	CAGAGACACAGACAAAGGGCTCCTCCGTTCTTCCACGCCAAAGGGCGACATGTGACGAG	808
Db	366	CAGAGACACAGACAAAGGGCTCCTCCGTTCTTCCACGCCAAAGGGCGACATGTGACGAG	307
QY	809	TCATATGATTAATCTTTGTGAAATTTGCACATGGAATTTGAAACATCTGAATCAGGGTATG	868
Db	306	TCATATGATTAATCTTTGTGAAATTTGCACATGGAATTTGAAACATCTGAATCAGGGTATG	247
QY	869	AAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCTGGAGAAATCTTCTGTGGACAT	928
Db	246	AAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCTGGAGAAATCTTCTGTGGACAT	187
QY	929	CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTCCCATGGGCATCTGGCCACCAAG	988

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Db 186 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTGCCATGGGCATCTGGCCACCAAG 127
Qy 989 GAAATTCGCACCTGACGATTAATCTTGACACTTTTATGTAATTCATTTGTTTATATGAT 1048
Db 126 GAAATTCGCACCTGACGATTAATCTTGACACTTTTATGTAATTCATTTGTTTATATGAT 67
Qy 1049 TTTCTCTAACATCAATTTAATGATGCTCTCGAATCTACTTTTTTATAAAAA 1103
Db 66 TTTCTCTAACATCAATTTAATGATGCTCTCGAATCTACTTTTTTATAAAAA 12

RESULT 6
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LOCUS 603190533F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261840 5',
DEFINITION mRNA sequence.
ACCESSION BI553612
VERSION BI553612.1 GI:15440924
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11660 row: a column: 09
High quality sequence stop: 742.
Location/Qualifiers
1. .906
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/clone="IMAGE:5261840"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
Query Match 61.1%; Score 691.4; DB 4; Length 906;
Best Local Similarity 97.9%; Pred. No. 6.4e-177;
Matches 753; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

Qy 75 CCACGAAGCCCTTCTCTCCGAGCGCGCGGTTTCGGCTTTGGGGGGGGGGGTACAG 134
Db 24 CCGGACGCGCGTTCTCTCTCCGAGCGCGCGGTTTCGGCTTTGGGGGGGGGGGTACAG 83
Qy 135 CCATCCATGACATGGGGGCAAGAGAGCCCGACCGCCCAAAAAAGACAGCGAAACC 194
Db 84 CCATCCATGACATGGGGGCAAGAGAGCCCGACCGCCCAAAAAAGACAGCGAAACC 143
Qy 195 TGCCCGCAGACGAAGGTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTGTGAAGC 254

Db 144 TGCCCGCAGACGAAGGTTTGGGATTTGTAGCGTCTGCACCTTCAGAAAACAGTGTGAAGC 203
Qy 255 CTTTAAATGCAAGCATCTCGGATGTGAGAAAGGACCTCCACGAGAAACCTCGGATCAA 314
Db 204 CTTTAAATGCAAGCATCTCGGATGTGAGAAAGGACCTCCACGAGAAACCTCGGATCAA 263
Qy 315 TTCTCAGCTGGTGGCACAACAAGTGGCAACAGTATGCCACCCCAACCCCTTAAAAA 374
Db 264 TTCTCAGCTGGTGGCACAACAAGTGGCAACAGTATGCCACCCCAACCCCTTAAAAA 323
Qy 375 GGAGAAGAAGGAGAAAAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAGCAAGGAAT 434
Db 324 GGAGAAGAAGGAGAAAAGTTGAAAAGCAGGACAAAAGAGAAAACCTGAGAAAGCAAGGAAT 383
Qy 435 TAGTCTCTAGTGTATACCAAGAAAATAACCAACAAGAAAACCAAAACCAAGTCTGACATTCT 494
Db 384 TAGTCTCTAGTGTATACCAAGAAAATAACCAACAAGAAAACCAAAACCAAGTCTGACATTCT 443
Qy 495 GAAAGATCCTCCTAGTGAAGCAACAGACATACAGTCTGCAAAATCTCAACAAAGACCCAG 554
Db 444 GAAAGATCCTCCTAGTGAAGCAACAGACATACAGTCTGCAAAATCTCAACAAAGACCCAG 503
Qy 555 CGAAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTGGACAGGACACTGCACAGCA 614
Db 504 CGAAACAAATCACACCTCAAGGCCCGCGCTGAAAAACGTGGACAGGACACTGCACAGCA 563
Qy 615 GTTGGCAGTAACTGTGGGCAACGTCACGTCATTATACAGACTTTAAGGAAAAGACTCG 674
Db 564 GTTGGCAGTAACTGTGGGCAACGTCACGTCATTATACAGACTTTAAGGAAAAGACTCG 623
Qy 675 CTCCTCATCGACATCTTCATCC-ACAGTGACCTCCAGTGAGGGTTCAGAACAGCAGAACCC 733
Db 624 CTCCTCATCGACATCTTCATCC-ACAGTGAGCTCCAGTGAGGGTTCAGAACAGCAGAACCC 683
Qy 734 AGAGCAGCTCGGGGTTCAGAGACACAGA-CAAGGGCTCTCTCCCGTTCT-CCACGCCAAA 791
Db 684 AGAGCAGCTC-GGGTTCAGAGACACAGACCAAGGGCTCTCTCCCGTTCTCTCCACGCCAAA 742
Qy 792 GGGGACATGTACAGCTCAATGATGATCTTTGTGAANTGCACATGG 840
Db 743 GGGGACATGTACAG-GTCCATGATGATCTCTCTGACATTTGCCCTTGG 790

RESULT 7
BI553612
LOCUS 60944142F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960195 5',
DEFINITION mRNA sequence.
ACCESSION BE300021
VERSION BE300021.1 GI:9183769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM53 row: c column: 12
High quality sequence stop: 713.
Location/Qualifiers
1. .936
/organism="Homo sapiens"

FEATURES
source
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/clone="IMAGE:2960195"
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/clone_lib="NIH_MGC_17"
/site="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8Kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 59.5%; Score 672.6; DB 2; Length 936;
Best Local Similarity 93.3%; Pred. No. 8.6e-172;
Matches 770; Conservative 0; Mismatches 44; Indels 11; Gaps 6;

QY 75 CCAAGAGGCTTCTCTCCGAGCGGCGCGTTCGGCTTGGGGGGGGGTACAG 134
DB CCGGACGCGGTTCTCTCCGAGCGGCGCGTTCGGCTTGGGGGGGGGTACAG 126
QY 135 CCATCCATGACATGGGCGCAAGAAGAGCCGACCGCCCAAAAGACGAGAAACC 194
DB CCATCCATGACATGGGCGCAAGAAGAGCCGACCGCCCAAAAGACGAGAAACC 186
QY 195 TGCCGAGAGGAGGTTTGGATGTTAGCGTCTGACCTTCAGAAACAGTGTGAAGC 254
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QY 255 CTTTAAATCAGCATCTGATGTGGAAGGCACTCCACGAGAAACCTCGATCAA 314
DB CTTTAAATCAGCATCTGATGTGGAAGGCACTCCACGAGAAACCTCGATCAA 306
QY 315 TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 374
DB TTCTCAGCTGGTGGCAACAAGTGGCAACAAGTATGCCACCCACACCCCTTAAAAA 366
QY 375 GGAGAGAGAGGAGAAAGTTGNAAGCAGGACCAAGAGAACTGTGAGAAAGACAAGAAAT 434
DB GGAGAGAGAGGAGAAAGTTGNAAGCAGGACCAAGAGAACTGTGAGAAAGACAAGAAAT 426
QY 435 TAGTCTAGTGTACCAAGAAAATACCAAGAGAAACCAACCAAGTCTGACATTC 494
DB TAGTCTAGTGTACCAAGAAAATACCAAGAGAAACCAACCAAGTCTGACATTC 486
QY 495 GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAG 554
DB GAAAGATCTCTTAGTGAAGCAACAGCATACAGTCTGCAAAATGCTACAAAGACCAAG 546
QY 555 CGAAACAAATACACCTCAAGGCCCGGTGAAAAACGTGGACAGGACACTGCAAGCA 614
DB CGAAACAAATACACCTCAAGGCCCGGTGAAAAACGTGGACAGGACACTGCAAGCA 606
QY 615 GTTGGCAGTAACCTGTGGGCAACGTACCGTCTATTATCAGAGCTTTAAG-GAAGAGCTC 673
DB GTTGGCAGTAACCTGTGGGCAACGTACCGTCTATTATCAGAGCTTTAAGTGAAGAGCTC 666
QY 674 GCTCCTCAGCATCTCTATCCACAGTGCACCTCCAGTGCAGGCTCAGAACGAGAAC 733
DB GCTCCTCAGCATCTCTATCCACAGTGCACCTCCAGTGCAGGCTCAGAACGAGAAC 725
QY 734 AGAGCAG- - - -CTCGGGGTGAGAGACACAGCAA- -GGGCTCTCTCCCGTTCCTCCAGCC 788
DB AGAGCAGCATACTCGGGGTCCAGAGAGACACAGCAAGGGGCTCTCTCCCGTTCCTCCAGCC 785
QY 789 AAGGGGGAATGT- - -CAGCAGTCAATGATGAATCTTTGTGAAATGACATGGAAATTG 845
DB AATGGGCGAAATGATCAAGCAGCTCATGATGAATCTTCTGGAATTTGGCAATGGGAATTG 845
QY 846 TGAAACTATGATCAGGGTATGAATTCAAATTCAAACCTCCACCTGCC 890

846 TG-ACACTATGATCCGGGAATTGACTCCAGACACAACTGCC 899

DB

RESULT 8
BX924636
LOCUS
DEFINITION
BX924636 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0017d.d.20 5prim, mRNA sequence.
ACCESSION
BX924636
VERSION
BX924636.1 GI:41141484
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 707)
AUTHORS
Bonnert,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
Soares,M., Bonaldo,F. and Hately,F.
TITLE
A Pig Normalised Multi-Tissue cDNA Library
JOURNAL
Unpublished (2003)
COMMENT
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0017 row: d column: 20.
Location/Qualifiers
1..707
/organism="Sus scrofa"
/mol_type="mrna"
/db_xref="taxon:9823"
/clone="scan0017d.d.20"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adnais, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

FEATURES
source

ORIGIN

Query Match 59.4%; Score 671.8; DB 5; Length 707;
Best Local Similarity 96.9%; Pred. No. 1.3e-171;
Matches 685; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 391 GTTGAAGAGCAGGACCAAGAGAAACCTGAGAAAGCAAGGAATTTAGTCTAGTGTACC 450
DB 1 GTTGAAGAGCAGATTAAGAGAAACCAAGAGAAATAGGAATTTAGTCTAGTGTACC 60
QY 451 AAGAAAAATACCAAGAAAAACCAAAAGTCTGACATTTCTGAAGATCTCTCTAGT 510
DB 61 AAGAAAAATACCAAGAAAAACCAAAAGTCTGATTTCTGAAGATCCACTAGT 120
QY 511 GAAGCAAAACAGCATACAGTCTGCAAAATGCTACAAAGAGACGAGCAAAATACACACC 570
DB 121 GAAGCAAAACAGPATACAGTTCAGCAATGCCAAGAGACGATGAAGCAATACACT 180
QY 571 TCAAGGCCCCGCTGAAAAACCGTGACAGGAGCACTGCAACAGAGTTGACAGTAACGTG 630
DB 181 TCAAGGCCCCGCTGAAAAACCGTGACAGGAGCACTGCAACAGAGTTGACAGTAACGTG 240
QY 631 GGCACAGTCACCGTCAATTATCAACAGTTTAAAGGAAAGACTCGCTCTCATCGACATCC 690


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QY 775 CGTTCCTCCAGCCCAAGGGGACATGTGACAGTCAATGATGATCTTTGTGA 828
Db 601 CTTTTCTCCAGCCCAAGGGGACATGTGACAGTCAATGATGATCTTTCTGA 654

RESULT 13
BQ015219/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ015219 662 bp mRNA linear EST 26-MAR-2002
UI-H-ED1-axw-f-13-0-UI.s1 NCI_CGAP_Ed1 Homo sapiens cDNA clone
IMAGE:5834508 3', mRNA sequence.
BQ015219
BQ015219.1 GI:19740120
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 662)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-23, >AT-rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5834508"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ed1"
/note="Organ: Left Pubic Bone, Vector: p7T73-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP Ed1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C85. The library was constructed according to
Bonald, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into p7T73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_lig=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN
Query Match 57.0%; Score 645.2; DB 5; Length 662;
Best Local Similarity 99.4%; Pred. No. 2.3e-164;
Matches 647; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 453 GAAATATACCAAGAAACCAAAAGTCTGACATCTTGAAGATCTCTTAGTGA 512
Db 662 GAAATATACCAAGAAACCAAAAGTCTGACATCTTGAAGATCTCTTAGTGA 603
QY 513 AGCAACAGCATACATCTGCAATGCTACACAAAGACCGGAAACAAATCACACCTC 572
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Db 602 AGCAACAGCATACATCTGCAATGCTACAAAGACCGGAAACAAATCACACCTC 543
QY 573 AAGSCCCCGGCTGAAAACAGTGGACAGGACATGCAAGAGTTGGCAGTAACTGTGGG 632
Db 542 AAGSCCCCGGCTGAAAACAGTGGACAGGACATGCAAGAGTTGGCAGTAACTGTGGG 483
QY 633 CAACGTCACCGTCATTATCAAGAAAAGACTCTTAAAGAAAAGACTCGCTCCTCATCGACATCCTC 692
Db 482 CAACGTCACCGTCATTATCAAGAAAAGACTCTTAAAGAAAAGACTCGCTCCTCATCGACATCCTC 423
QY 693 ATCCACAGTACCTCCAGTGCAGGCTCAGAACACAGACAGACCTCGGGGTGAGA 752
Db 422 ATCCACAGTACCTCCAGTGCAGGCTCAGAACACAGACAGACCTCGGGGTGAGA 363
QY 753 GAGCACAGACAAAGGGCTCCTCCGCTTCTCCACGCCAAAGGGCGACATGTGACAGTCAA 812
Db 362 GAGCACAGACAAAGGGCTCCTCCGCTTCTCCACGCCAAAGGGCGACATGTGACAGTCAA 303
QY 813 TGATGAATCTTTGTGAAATTGACATGCAATGGAATTGTGAAAACCTATGAATCAGGGTATGAAAT 872
Db 302 TGATGAATCTTTGTGAAATTGACATGCAATGGAATTGTGAAAACCTATGAATCAGGGTATGAAAT 243
QY 873 TCAAAAACCTCCACCTGCCATGCTGCTTGCATCCCTCGAGAAATCTTCTGTGGACATCGAC 932
Db 242 TCAAAAACCTCCACCTGCCATGCTGCTTGCATCCCTCGAGAAATCTTCTGTGGACATCGAC 183
QY 933 CTCTTAGTGAGTGCAGGAGTAATTTCTGCTGCATGGGCATCTGGCCACCAAGGAAT 992
Db 182 CTCTTAGTGAGTGCAGGAGTAATTTCTGCTGCATGGGCATCTGGCCACCAAGGAAT 123
QY 993 TTGCGACCCCTGACGATTAATCTTGCACATTTATGATATTCATTTATATGATTTTC 1052
Db 122 TTGCGACCCCTGACGATTAATCTTGCACATTTATGATATTCATTTATATGATTTTC 63
QY 1053 CTAAACATCATTTATATTAATGGATGCTCCTCGAATCTCTTTTATATAAAA 1103
Db 62 CTAAACATCATTTATATTAATGGATGCTCCTCGAATCTCTTTTATATAAAA 12

RESULT 14
CK299391 664 bp mRNA linear EST 15-DEC-2003
UI-E-EJ1-ajv-e-08-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
DEFINITION
UI-E-EJ1-ajv-e-08-0-UI 3', mRNA sequence.
ACCESSION
CK299391
VERSION
CK299391.1 GI:39887700
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
Bonald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
9704477
MEDLINE
8889548
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Greg Hageman
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/eye.html
The following repetitive elements were found in this cDNA
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sequence: 1-23, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..664
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajv-e-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCOCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG LIB=UI-E-EJ1
TAG_SEQ=AGAATCAAGA"

ORIGIN

Query Match 56.1%; Score 634; DB 7; Length 664;
Best Local Similarity 99.2%; Pred. No. 2.6e-161;
Matches 637; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 462 CAACAGAAAACCAACCAAGCTGTGACATCTCGAAGATCTCTCTAGTGAAGCAACAG 521
DB 653 CGAGAGAAACCAACCAAGCTGTGACATCTCGAAGATCTCTCTAGTGAAGCAACAG 594
QY 522 CATACAGTCTGCAATGTCTACAAAGAACCCAGCGAAGCAAAATCACCTCAAGSCCCCG 581
DB 593 CATACAGTCTGCAATGTCTACAAAGAACCCAGCGAAGCAAAATCACCTCAAGSCCCCG 534
QY 582 GCTGAAAACGTGGACAGAGACATGCGACAGAGTTGGCAGTAACTGTGGGCAACGTAC 641
DB 533 GCTGAAAACGTGGACAGAGACATGCGACAGAGTTGGCAGTAACTGTGGGCAACGTAC 474
QY 642 CGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCTCATCCACAGT 701
DB 473 CGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCTCATCCACAGT 414
QY 702 GACCTCCAGTGCAGGCTCAGAACAGACAGACAGAGCTCGGGTTCAGAGAGCACAGA 761
DB 413 GACCTCCAGTGCAGGCTCAGAACAGACAGACAGAGCTCGGGTTCAGAGAGCACAGA 354
QY 762 CAAGGGCTCTCCGTTCTCCACGCCAAAGGGCGACATGTGCAGAGTCAATGATGATC 821
DB 353 CAAGGGCTCTCCGTTCTCCACGCCAAAGGGCGACATGTGCAGAGTCAATGATGATC 294
QY 822 TTGTGAAATTCACATGAATTTGTGAAACCTATCAATCAGGGTATGAAATTCAGAACT 881
DB 294 TTGTGAAATTCACATGAATTTGTGAAACCTATCAATCAGGGTATGAAATTCAGAACT 234
QY 882 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGT 941
DB 233 CCACCTGCCCATGCTGCTTGCATCCCTGGAGAAATCTTCTGTGGACATCGACCTCTTAGT 174

QY 942 ATGCTGCCAGGATAATTTCTGCTTGCCATGGCCATCGGCACCAAGAAATTTTCGCACCC 1001
DB 173 ATGCTGCCAGGATAATTTCTGCTTGCCATGGCCATCGGCACCAAGAAATTTTCGCACCC 114
QY 1002 TGACGATTAATCTCTTGACACATTTTATGTATTCATTTGTTTATATGATTTTCTAACATC 1061
DB 113 TGACGATTAATCTCTTGACACATTTTATGTATTCATTTGTTTATATGATTTTCTAACATC 54
QY 1062 ATTTATTAATGGATGTGCTCTCGAATCTACTTTTATAAATA 1103
DB 53 ATTTATTAATGGATGTGCTCTCGAATCTACTTTTATAAATA 12

RESULT 15
LOCUS BQ189224
DEFINITION UI-E-EJ1-ajv-e-08-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
ACCESSION BQ189224
KEYWORDS BQ189224.1 GI:20364775
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 650)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 626-650, >AT rich#Low_complexity (matched complicity)
Seq primer: M13 REVERSE.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajv-e-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 09:29:36 ; Search time 218.254 Seconds
(without alignments)
8479.259 Million cell updates/sec

Title: US-09-655-109A-5

Perfect score: 1131

Sequence: 1 tataactatctatctgatga.....tggcctcgagagatctatga 1131

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152.6	13.5	376	4	US-09-513-999C-3095 Sequence 3095, Ap
2	105.6	9.4	466	4	US-09-621-976-2061 Sequence 2061, Ap
3	74	6.5	1039	3	US-09-269-617-11 Sequence 11, Appl
4	73	6.5	231	3	US-09-012-515A-20 Sequence 20, Appl
5	73	6.5	231	3	US-08-360-144A-20 Sequence 20, Appl
6	73	6.5	231	3	US-09-012-504A-20 Sequence 20, Appl
7	73	6.5	231	4	US-09-012-399A-20 Sequence 20, Appl
8	73	6.5	231	5	PCT-US95-06722-20 Sequence 13, Appl
9	71	6.3	1025	3	US-09-269-617-13 Sequence 14, Appl
10	59.2	5.2	7218	1	US-08-232-463-14 Sequence 29, Appl
11	56.8	5.0	288	3	US-09-025-151-29 Sequence 29, Appl
12	56.8	5.0	288	4	US-09-637-240-29 Sequence 29, Appl
13	55.8	4.9	1206	1	US-08-318-947A-1 Sequence 1, Appl
14	55.8	4.9	1206	2	US-08-795-303-1 Sequence 1, Appl
15	55	4.9	612	4	US-09-620-312D-529 Sequence 529, App
16	55	4.9	659	4	US-09-620-312D-634 Sequence 634, App
17	55	4.9	668	4	US-09-620-312D-198 Sequence 198, App
18	55	4.9	771	4	US-09-620-312D-1043 Sequence 1043, App
19	55	4.9	771	4	US-09-620-312D-1043 Sequence 1043, App
20	55	4.9	783	4	US-09-620-312D-701 Sequence 701, App
21	55	4.9	827	4	US-09-620-312D-522 Sequence 522, App
22	55	4.9	1163	4	US-09-620-312D-250 Sequence 250, App
23	55	4.9	1196	4	US-09-620-312D-906 Sequence 906, App
24	55	4.9	1239	4	US-09-620-312D-663 Sequence 663, App
25	55	4.9	1239	4	US-09-620-312D-663 Sequence 663, App
26	55	4.9	1477	4	US-09-620-312D-627 Sequence 627, App
27	55	4.9	1572	4	US-09-620-312D-886 Sequence 886, App

ALIGNMENTS

RESULT 1

US-09-513-999C-3095
; Sequence 3095, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCES: 59 US2 REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 3095

; LENGTH: 376

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 69..374

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 367

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 100

; OTHER INFORMATION: Xaa=Lys or Thr

US-09-513-999C-3095

Query Match 13.5%; Score 152.6; DB 4; Length 376;

Best Local Similarity 66.7%; Pred. No. 7.3e-37;

Matches 218; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Sequence 177, App
Sequence 593, App
Sequence 60, Appl
Sequence 172, App
Sequence 68, Appl
Sequence 800, App
Sequence 799, App
Sequence 143, App
Sequence 167, App
Sequence 30, Appl
Sequence 280, App
Sequence 347, App
Sequence 678, App
Sequence 679, App
Sequence 677, App
Sequence 298, App
Sequence 332, App

QY 125 CGGGGTACGCCCATCCATGACCATGGCGGACAGAGAGCCCGACCGAGGAGAGAC 184
DB 46 CGGGTGGGTGATAGCCAGCCATGGAGACAGAGAGCCCGACCGAGGAGCGGC 105
QY 185 AAGCGAAACCTGGCGGACAGAGAGGGTTTGGGATTGTAGCGTCTGCACCTTGAACA 244
DB 106 AGCCGAAGCCGTCCTCGATGAGGGTTACTGGGACTGTAGCGTCTGCACCTTCGGA 165
QY 245 GTGCTGAAGCCTTTAAATGCGCATCTCGATGTGAGAAAGGAGGACCTCCACCAAGAAAC 304
DB 166 GCGCCGAGGCGCTTCAAGTGATGATGTGCGAAGGAGGACCTCCACCGGAAAC 225


```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 128
; OTHER INFORMATION: /label= XhoI
US-09-012-515A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133

RESULT 6
US-09-012-504A-20
; Sequence 20, Application US/09012504A
; Patent No. 6464974
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, I.
; APPLICANT: Cottarel, G.
; APPLICANT: Damagnez, V.
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; FILE REFERENCE: APBI-P05-036
; CURRENT APPLICATION NUMBER: US/09/012,504A
; CURRENT FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 08/360,144
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/250,795
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Mammalian
US-09-012-504A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133

RESULT 7
US-09-012-399A-20
; Sequence 20, Application US/09012399A
; Patent No. 6509152
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,399A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-036.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 128
; OTHER INFORMATION: /label= XhoI
US-08-360-144A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133

RESULT 5
US-08-360-144A-20
; Sequence 20, Application US/08360144A
; Patent No. 6150137
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,144A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-036.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 128
; OTHER INFORMATION: /label= XhoI
US-08-360-144A-20

Query Match 6.5%; Score 73; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 60
DB 61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAGAGATCTGGAAT 120

QY 61 TCGGATCCTCGAG 73
DB 121 TCGGATCCTCGAG 133
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Query Match          6.5%; Score 73; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCCAAAAAAGAGATCTCGAAT 60
        |||||
Dd      61 TATAACTATCTATTTCGATGATGAAGATACCCCAACCAACCCAAAAAAGAGATCTCGAAT 120
        |||||

QY      61 TCGGATCCTCGAG 73
        |||||
Dd      121 TCGGATCCTCGAG 133

RESULT 9
US-09-269-617-13
; Sequence 13, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,617
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 base pairs

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: B-lymphocyte
; IMMEDIATE SOURCE:
; LIBRARY: Human cDNA library
; CLONE: SZ33
; US-09-269-617-13

Query Match 6.3%; Score 71; DB 3; Length 1025;
Best Local Similarity 92.4%; Pred. No. 2.9e-11;
Matches 85; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 TATACTATCTATTTCGATGATGAAGATACCCACCAAAACCCAAAAAAGAGATCTCGAAT 60
DB 35 TATATACCTCTATTTCGATGATGAAGATA-CCCAACCAACCCAAAAAAGAGATCTCGAAT 93
QY 61 TCGGATCCTCGAGGCCACGAAGGCCTTTCTCC 92
DB 94 TCGGATCCTCGAGGCCACGANGCCGGCCTTC 125

RESULT 10
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500

```


GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; NUMBER OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..648
US-08-318-947A-1

Query Match 4.9%; Score 55.8; DB 1; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.7e-06;
Matches 63; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 31 CCACCAAAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90
Db 1 CCACCAAAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90

Qy 91 CCTCCGAGCGGCC 105
Db 61 CTCGGAGGGAAGTC 75

RESULT 14
US-08-795-303-1
; Sequence 1, Application US/08795303
; Patent No. 5948656
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; NUMBER OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC

COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 172..648
US-08-795-303-1

Query Match 4.9%; Score 55.8; DB 2; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.7e-06;
Matches 63; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 31 CCACCAAAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90
Db 1 CCACCAAAACCCAAAGAGATCTGGAATTCGGATCTCGAGGCCACGAAGCCCTTCT 90

Qy 91 CCTCCGAGCGGCC 105
Db 61 CTCGGAGGGAAGTC 75

RESULT 15
US-09-620-312D-529
; Sequence 529, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides

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; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620.312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PC_FL_genes Version 1.0
; SEQ ID NO 529
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (118)..(486)
US-09-620-312D-529

Query Match          4.9%; Score 55; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAAAGAGATCT 55
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Db      20 TATAACTATCTATTTCGATGATGAAGATACCCCAACCCCAAAAAAGAGATCT 74

Search completed: September 11, 2005, 15:33:26
Job time : 220.254 secs

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